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SEQUENCE LISTING

<110> Adra, Chaker

<120> GRANULOCYTE SUBTYPE-SELECTIVE RECEPTORS AND ION CHANNELS AND USES THEREOF

<130> A0852.70000WO00

<140> Not yet assigned

<141> 2005-03-03

<150> 60/549,865

<151> 2004-03-03

<160> 31

<170> PatentIn version 3.3

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Gly Tyr Gly Val Arg Ser Ile Thr Glu Glu Cys Pro His Ala Ile Phe
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Gly Gln Arg Tyr Leu Ala Asp Ile Phe Thr Thr Cys Val Asp Ile Arg
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acc acc ccg gtc gtc atc gtc gtg tac ctg tcc aag cag cgt tgg gag Thr Thr Pro Val Val Ile Val Val Tyr Leu Ser Lys Gln Arg Trp Glu 110 115 120			570
cac atc gac ccg tcg ggg cgg ctc tgc acc ttt ttc ggg ctg acc atg His Ile Asp Pro Ser Gly Arg Leu Cys Thr Phe Phe Gly Leu Thr Met 125 130 135			618
act gtt ttc ggg ctc tcc tcg ttg ttc atc gcc agc gcc atg gcc gtc Thr Val Phe Gly Leu Ser Ser Leu Phe Ile Ala Ser Ala Met Ala Val 140 145 150			666
gag cgg gcg ctg gcc atc agg gcg ccg cac tgg tat gcg agc cac atg Glu Arg Ala Leu Ala Ile Arg Ala Pro His Trp Tyr Ala Ser His Met 155 160 165			714
aag acg cgt gcc acc cgc gct gtg ctg ctc ggc gtg tgg ctg gcc gtg Lys Thr Arg Ala Thr Arg Ala Val Leu Leu Gly Val Trp Leu Ala Val 170 175 180 185			762
ctc gcc ttc gcc ctg ctg ccg gtg ctg ggc gtg ggc cag tac acc gtc Leu Ala Phe Ala Leu Leu Pro Val Leu Gly Val Gly Gln Tyr Thr Val 190 195 200			810
cag tgg ccc ggg acg tgg tgc ttc atc agc acc ggg cga ggg ggc aac Gln Trp Pro Gly Thr Trp Cys Phe Ile Ser Thr Gly Arg Gly Gly Asn 205 210 215			858
ggg act agc tct tcg cat aac tgg ggc aac ctt ttc ttc gcc tct gcc Gly Thr Ser Ser Ser His Asn Trp Gly Asn Leu Phe Phe Ala Ser Ala 220 225 230			906
ttt gcc ttc ctg ggg ctc ttg gcg ctg aca gtc acc ttt tcc tgc aac Phe Ala Phe Leu Gly Leu Leu Ala Leu Thr Val Thr Phe Ser Cys Asn 235 240 245			954
ctg gcc acc att aag gcc ctg gtg tcc cgc tgc cgg gcc aag gcc acg Leu Ala Thr Ile Lys Ala Leu Val Ser Arg Cys Arg Ala Lys Ala Thr 250 255 260 265			1002
gca tct cag tcc agt gcc cag tgg ggc cgc atc acg acc gag acg gcc Ala Ser Gln Ser Ser Ala Gln Trp Gly Arg Ile Thr Thr Glu Thr Ala 270 275 280			1050
att cag ctt atg ggg atc atg tgc gtg ctg tcg gtc tgc tgg tct ccg Ile Gln Leu Met Gly Ile Met Cys Val Leu Ser Val Cys Trp Ser Pro 285 290 295			1098
ctc ctg ata atg atg ttg aaa atg atc ttc aat cag aca tca gtt gag Leu Leu Ile Met Met Leu Lys Met Ile Phe Asn Gln Thr Ser Val Glu 300 305 310			1146

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cac tgc aag aca cac acg gag aag cag aaa gaa tgc aac ttc ttc tta      1194
His Cys Lys Thr His Thr Glu Lys Gln Lys Glu Cys Asn Phe Phe Leu
      315                      320                      325

ata gct gtt cgc ctg gct tca ctg aac cag atc ttg gat cct tgg gtt      1242
Ile Ala Val Arg Leu Ala Ser Leu Asn Gln Ile Leu Asp Pro Trp Val
      330                      335                      340                      345

tac ctg ctg tta aga aag atc ctt ctt cga aag ttt tgc cag atc agg      1290
Tyr Leu Leu Leu Arg Lys Ile Leu Leu Arg Lys Phe Cys Gln Ile Arg
                        350                      355                      360

tac cac aca aac aac tat gca tcc agc tcc acc tcc tta ccc tgc cag      1338
Tyr His Thr Asn Asn Tyr Ala Ser Ser Ser Thr Ser Leu Pro Cys Gln
                        365                      370                      375

tgt tcc tca acc ttg atg tgg agc gac cat ttg gaa aga taa      1380
Cys Ser Ser Thr Leu Met Trp Ser Asp His Leu Glu Arg
      380                      385                      390

tgaaagaacg gagttggaca ttttattgca attcctgctt ccctgaattt gcatatttct      1440

tcccacctga gaaggataat tatataatttt aatttggatt atttcttcat ttttatcttt      1500

ttatttttaat gattgttttg tcagtaatac ccatggagat caactttatt attataatcc      1560

atgcctctga atattagagg gtttcttgga tgggattttg aatatgcatt taagaacggt      1620

gggaacaatt tcacagatga tgattggagg aaaagtgatg aaaagaaaga cctgtgttcc      1680

aggagttttc tccaacttca aacctttacg tgaatcttaa ccaaagtgga catctttaca      1740

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gaaaagtcaa catattgaga gtgataattc aattaatagg atatgaactt aacgacatat      1860

aaaagataaa cttaacgaca tataaaagca aataagggca ggagggaatc gtgacaaaaa      1920

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gaactaaaag ttctaagtct caattctagt tatgtgtcat ttagtaactc aggaatctgc      2040

ttaattgtta tttctaagct tttgatgaca aaggagtgat gcagctaagg gcatccttgg      2100

agtgtcataa aaaacaaatt tgaggttgaa tgattagctg ccagttagag tgataaaaaa      2160

atccaggtag gccttctgat tcaccatgac caagtcagga tttcttaata tttcttttct      2220

ggcagcatat acaaaggcaa aattaataaa taacagttgt tgaataacaa actttattac      2280

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ctaa                                                                2344

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<212> PRT
<213> Homo sapiens

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- 14 -

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Ala	Arg	Gly	Asn	Leu	Thr	Arg	Pro	Pro	Gly	Ser	Gly	Glu	Asp	Cys	Gly	35	40	45	
Ser	Val	Ser	Val	Ala	Phe	Pro	Ile	Thr	Met	Leu	Leu	Thr	Gly	Phe	Val	50	55	60	
Gly	Asn	Ala	Leu	Ala	Met	Leu	Leu	Val	Ser	Arg	Ser	Tyr	Arg	Arg	Arg	65	70	75	80
Glu	Ser	Lys	Arg	Lys	Lys	Ser	Phe	Leu	Leu	Cys	Ile	Gly	Trp	Leu	Ala	85	90	95	
Leu	Thr	Asp	Leu	Val	Gly	Gln	Leu	Leu	Thr	Thr	Pro	Val	Val	Ile	Val	100	105	110	
Val	Tyr	Leu	Ser	Lys	Gln	Arg	Trp	Glu	His	Ile	Asp	Pro	Ser	Gly	Arg	115	120	125	
Leu	Cys	Thr	Phe	Phe	Gly	Leu	Thr	Met	Thr	Val	Phe	Gly	Leu	Ser	Ser	130	135	140	
Leu	Phe	Ile	Ala	Ser	Ala	Met	Ala	Val	Glu	Arg	Ala	Leu	Ala	Ile	Arg	145	150	155	160
Ala	Pro	His	Trp	Tyr	Ala	Ser	His	Met	Lys	Thr	Arg	Ala	Thr	Arg	Ala	165	170	175	
Val	Leu	Leu	Gly	Val	Trp	Leu	Ala	Val	Leu	Ala	Phe	Ala	Leu	Leu	Pro	180	185	190	
Val	Leu	Gly	Val	Gly	Gln	Tyr	Thr	Val	Gln	Trp	Pro	Gly	Thr	Trp	Cys	195	200	205	
Phe	Ile	Ser	Thr	Gly	Arg	Gly	Gly	Asn	Gly	Thr	Ser	Ser	Ser	His	Asn	210	215	220	
Trp	Gly	Asn	Leu	Phe	Phe	Ala	Ser	Ala	Phe	Ala	Phe	Leu	Gly	Leu	Leu	225	230	235	240
Ala	Leu	Thr	Val	Thr	Phe	Ser	Cys	Asn	Leu	Ala	Thr	Ile	Lys	Ala	Leu	245	250	255	

Cys Val Leu Ser Val Cys Trp Ser Pro Leu Leu Ile Met Met Leu Lys
290 295 300

Met Ile Phe Asn Gln Thr Ser Val Glu His Cys Lys Thr His Thr Glu
305 310 315 320

Lys Gln Lys Glu Cys Asn Phe Phe Leu Ile Ala Val Arg Leu Ala Ser
325 330 335

Leu Asn Gln Ile Leu Asp Pro Trp Val Tyr Leu Leu Leu Arg Lys Ile
340 345 350

Leu Leu Arg Lys Phe Cys Gln Ile Arg Tyr His Thr Asn Asn Tyr Ala
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370 375 380

Ser Asp His Leu Glu Arg
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<212>    DNA
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 Met Arg Gly Phe Asn Leu
 1 5

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Leu	Leu	Phe	Trp	Gly	Cys	Cys	Val	Met	His	Ser	Trp	Glu	Gly	His	Ile	
			10				15						20			

aga ccc aca cgg aaa cca aac aca aag ggt aat aac tgt aga gac agt 152
Arg Pro Thr Arg Lys Pro Asn Thr Lys Gly Asn Asn Cys Arg Asp Ser
25 30 35

acc ttg tgc cca gct tat gcc acc tgc acc aat aca gtg gac agt tac 200

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Thr	Leu	Cys	Pro	Ala	Tyr	Ala	Thr	Cys	Thr	Asn	Thr	Val	Asp	Ser	Tyr	
40						45				50						
tat	tgc	gct	tgc	aaa	caa	ggc	ttc	ctg	tcc	agc	aat	ggg	caa	aat	cac	248
Tyr	Cys	Ala	Cys	Lys	Gln	Gly	Phe	Leu	Ser	Ser	Asn	Gly	Gln	Asn	His	
55					60					65					70	
ttc	aag	gat	cca	gga	gtg	cga	tgc	aaa	gat	att	gat	gaa	tgt	tct	caa	296
Phe	Lys	Asp	Pro	Gly	Val	Arg	Cys	Lys	Asp	Ile	Asp	Glu	Cys	Ser	Gln	
				75					80					85		
agc	ccc	cag	ccc	tgt	ggc	cct	aac	tca	tcc	tgc	aaa	aac	ctg	tca	ggg	344
Ser	Pro	Gln	Pro	Cys	Gly	Pro	Asn	Ser	Ser	Cys	Lys	Asn	Leu	Ser	Gly	
			90					95					100			
agg	tac	aag	tgc	agc	tgt	tta	gat	ggc	ttc	tct	tct	ccc	act	gga	aat	392
Arg	Tyr	Lys	Cys	Ser	Cys	Leu	Asp	Gly	Phe	Ser	Ser	Pro	Thr	Gly	Asn	
		105					110					115				
gac	tgg	gtc	cca	gga	aag	ccg	ggc	aat	ttc	tcc	tgt	act	gat	atc	aat	440
Asp	Trp	Val	Pro	Gly	Lys	Pro	Gly	Asn	Phe	Ser	Cys	Thr	Asp	Ile	Asn	
	120					125					130					
gag	tgc	ctc	acc	agc	agc	gtc	tgc	cct	gag	cat	tct	gac	tgt	gtc	aac	488
Glu	Cys	Leu	Thr	Ser	Ser	Val	Cys	Pro	Glu	His	Ser	Asp	Cys	Val	Asn	
135					140					145					150	
tcc	atg	gga	agc	tac	agt	tgc	agc	tgt	caa	gtt	gga	ttc	atc	tct	aga	536
Ser	Met	Gly	Ser	Tyr	Ser	Cys	Ser	Cys	Gln	Val	Gly	Phe	Ile	Ser	Arg	
				155					160					165		
aac	tcc	acc	tgt	gaa	gac	gtg	gat	gaa	tgt	gca	gat	cca	aga	gct	tgc	584
Asn	Ser	Thr	Cys	Glu	Asp	Val	Asp	Glu	Cys	Ala	Asp	Pro	Arg	Ala	Cys	
			170					175					180			
cca	gag	cat	gca	act	tgt	aat	aac	act	gtt	gga	aac	tac	tct	tgt	ttc	632
Pro	Glu	His	Ala	Thr	Cys	Asn	Asn	Thr	Val	Gly	Asn	Tyr	Ser	Cys	Phe	
		185					190					195				
tgc	aac	cca	gga	ttt	gaa	tcc	agc	agt	ggc	cac	ttg	agt	ttc	cag	ggc	680
Cys	Asn	Pro	Gly	Phe	Glu	Ser	Ser	Ser	Gly	His	Leu	Ser	Phe	Gln	Gly	
	200					205					210					
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Leu	Lys	Ala	Ser	Cys	Glu	Asp	Ile	Asp	Glu	Cys	Thr	Glu	Met	Cys	Pro	
215					220					225					230	
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Ile	Asn	Ser	Thr	Cys	Thr	Asn	Thr	Pro	Gly	Ser	Tyr	Phe	Cys	Thr	Cys	
				235					240					245		
cac	cct	ggc	ttt	gca	cca	agc	aat	gga	cag	ttg	aat	ttc	aca	gac	caa	824
His	Pro	Gly	Phe	Ala	Pro	Ser	Asn	Gly	Gln	Leu	Asn	Phe	Thr	Asp	Gln	
			250					255					260			
gga	gtg	gaa	tgt	aga	gat	att	gat	gag	tgc	cgc	caa	gat	cca	tca	acc	872
Gly	Val	Glu	Cys	Arg	Asp	Ile	Asp	Glu	Cys	Arg	Gln	Asp	Pro	Ser	Thr	
		265					270					275				
tgt	ggc	cct	aat	tct	atc	tgc	acc	aat	gcc	ctg	ggc	tcc	tac	agc	tgt	920
Cys	Gly	Pro	Asn	Ser	Ile	Cys	Thr	Asn	Ala	Leu	Gly	Ser	Tyr	Ser	Cys	
	280					285					290					

- 17 -

ggc tgc att gca ggc ttt cat ccc aat cca gaa ggc tcc cag aaa gat	968
Gly Cys Ile Ala Gly Phe His Pro Asn Pro Glu Gly Ser Gln Lys Asp	
295 300 305 310	
ggc aac ttc agc tgc caa agg gtt ctc ttc aaa tgt aag gaa gat gtg	1016
Gly Asn Phe Ser Cys Gln Arg Val Leu Phe Lys Cys Lys Glu Asp Val	
315 320 325	
ata ccc gat aat aag cag atc cag caa tgc caa gag gga acc gca gtg	1064
Ile Pro Asp Asn Lys Gln Ile Gln Gln Cys Gln Glu Gly Thr Ala Val	
330 335 340	
aaa cct gca tat gtc tcc ttt tgt gca caa ata aat aac atc ttc agc	1112
Lys Pro Ala Tyr Val Ser Phe Cys Ala Gln Ile Asn Asn Ile Phe Ser	
345 350 355	
gtt ctg gac aaa gtg tgt gaa aat aaa acg acc gta gtt tct ctg aag	1160
Val Leu Asp Lys Val Cys Glu Asn Lys Thr Thr Val Val Ser Leu Lys	
360 365 370	
aat aca act gag agc ttt gtc cct gtg ctt aaa caa ata tcc acg tgg	1208
Asn Thr Thr Glu Ser Phe Val Pro Val Leu Lys Gln Ile Ser Thr Trp	
375 380 385 390	
act aaa ttc acc aag gaa gag acg tcc tcc ctg gcc aca gtc ttc ctg	1256
Thr Lys Phe Thr Lys Glu Glu Thr Ser Ser Leu Ala Thr Val Phe Leu	
395 400 405	
gag agt gtg gaa agc atg aca ctg gca tct ttt tgg aaa ccc tca gca	1304
Glu Ser Val Glu Ser Met Thr Leu Ala Ser Phe Trp Lys Pro Ser Ala	
410 415 420	
aat atc act ccg gct gtt cgg acg gaa tac tta gac att gag agc aaa	1352
Asn Ile Thr Pro Ala Val Arg Thr Glu Tyr Leu Asp Ile Glu Ser Lys	
425 430 435	
gtt atc aac aaa gaa tgc agt gaa gag aat gtg acg ttg gac ttg gta	1400
Val Ile Asn Lys Glu Cys Ser Glu Glu Asn Val Thr Leu Asp Leu Val	
440 445 450	
gcc aag ggg gat aag atg aag atc ggg tgt tcc aca att gag gaa tct	1448
Ala Lys Gly Asp Lys Met Lys Ile Gly Cys Ser Thr Ile Glu Glu Ser	
455 460 465 470	
gaa tcc aca gag acc act ggt gtg gct ttt gtc tcc ttt gtg ggc atg	1496
Glu Ser Thr Glu Thr Thr Gly Val Ala Phe Val Ser Phe Val Gly Met	
475 480 485	
gaa tcg gtt tta aat gag cgc ttc ttc aaa gac cac cag gct ccc ttg	1544
Glu Ser Val Leu Asn Glu Arg Phe Phe Lys Asp His Gln Ala Pro Leu	
490 495 500	
acc acc tct gag atc aag ctg aag atg aat tct cga gtc gtt ggg ggc	1592
Thr Thr Ser Glu Ile Lys Leu Lys Met Asn Ser Arg Val Val Gly Gly	
505 510 515	
ata atg act gga gag aag aaa gac ggc ttc tca gat cca atc atc tac	1640
Ile Met Thr Gly Glu Lys Lys Asp Gly Phe Ser Asp Pro Ile Ile Tyr	
520 525 530	
act ctg gag aac att cag cca aag cag aag ttt gag agg ccc atc tgt	1688

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Thr 535	Leu	Glu	Asn	Ile	Gln 540	Pro	Lys	Gln	Lys	Phe 545	Glu	Arg	Pro	Ile	Cys 550	
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Val	Ser	Trp	Ser	Thr 555	Asp	Val	Lys	Gly	Gly 560	Arg	Trp	Thr	Ser	Phe 565	Gly	
tgt	gtg	atc	ctg	gaa	gct	tct	gag	aca	tat	acc	atc	tgc	agc	tgt	aat	1784
Cys	Val	Ile	Leu	Glu 570	Ala	Ser	Glu	Thr 575	Tyr	Thr	Ile	Cys	Ser 580	Cys	Asn	
cag	atg	gca	aat	ctt	gcc	gtt	atc	atg	gcg	tct	ggg	gag	ctc	acg	atg	1832
Gln	Met	Ala	Asn	Leu	Ala	Val	Ile 590	Met	Ala	Ser	Gly	Glu 595	Leu	Thr	Met	
gac	ttt	tcc	ttg	tac	atc	att	agc	cat	gta	ggc	att	atc	atc	tcc	ttg	1880
Asp	Phe 600	Ser	Leu	Tyr	Ile	Ile 605	Ser	His	Val	Gly	Ile 610	Ile	Ile	Ser	Leu	
gtg	tgc	ctc	gtc	ttg	gcc	atc	gcc	acc	ttt	ctg	ctg	tgt	cgc	tcc	atc	1928
Val	Cys	Leu	Val	Leu	Ala 620	Ile	Ala	Thr	Phe	Leu 625	Leu	Cys	Arg	Ser	Ile 630	
cga	aat	cac	aac	acc	tac	ctc	cac	ctg	cac	ctc	tgc	gtg	tgt	ctc	ctc	1976
Arg	Asn	His	Asn	Thr 635	Tyr	Leu	His	Leu	His 640	Leu	Cys	Val	Cys	Leu 645	Leu	
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Leu	Ala	Lys	Thr 650	Leu	Phe	Leu	Ala	Gly 655	Ile	His	Lys	Thr	Asp 660	Asn	Lys	
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Cys	Phe 680	Phe	Trp	Met	Leu	Val 685	Glu	Ala	Val	Ile	Leu 690	Phe	Leu	Met	Val	
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Arg	Asn	Leu	Lys	Val	Val 700	Asn	Tyr	Phe	Ser	Ser 705	Arg	Asn	Ile	Lys 710	Met	
ctg	cac	atc	tgt	gcc	ttt	ggg	tat	ggg	ctg	ccg	atg	ctg	gtg	gtg	gtg	2216
Leu	His	Ile	Cys	Ala 715	Phe	Gly	Tyr	Gly 720	Leu	Pro	Met	Leu	Val 725	Val	Val	
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Ile	Ser	Ala	Ser 730	Val	Gln	Pro	Gln	Gly 735	Tyr	Gly	Met	His	Asn 740	Arg	Cys	
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Trp	Leu	Asn 745	Thr	Glu	Thr	Gly	Phe 750	Ile	Trp	Ser	Phe	Leu 755	Gly	Pro	Val	
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Cys	Thr	Val	Ile	Val	Ile	Asn 765	Ser	Leu	Leu	Leu	Thr 770	Trp	Thr	Leu	Trp	
atc	ctg	agg	cag	agg	ctt	tcc	agt	gtt	aat	gcc	gaa	gtc	tca	acg	cta	2408
Ile	Leu	Arg	Gln	Arg	Leu 780	Ser	Ser	Val	Asn	Ala 785	Glu	Val	Ser	Thr	Leu 790	

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ctg ggc tgc tcc tgg gtg ctg ggc att ttt cag att gga cct gtg gca      2504
Leu Gly Cys Ser Trp Val Leu Gly Ile Phe Gln Ile Gly Pro Val Ala
                        810                        815                        820

ggg gtc atg gct tac ctg ttc acc atc atc aac agc ctg cag ggg gcc      2552
Gly Val Met Ala Tyr Leu Phe Thr Ile Ile Asn Ser Leu Gln Gly Ala
                        825                        830                        835

ttc atc ttc ctc atc cac tgt ctg ctc aac ggc cag gta cga gaa gaa      2600
Phe Ile Phe Leu Ile His Cys Leu Leu Asn Gly Gln Val Arg Glu Glu
                        840                        845                        850

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Tyr Lys Arg Trp Ile Thr Gly Lys Thr Lys Pro Ser Ser Gln Ser Gln
855                        860                        865                        870

acc tca agg atc ttg ctg tcc tcc atg cca tcc gct tcc aag acg ggt      2696
Thr Ser Arg Ile Leu Leu Ser Ser Met Pro Ser Ala Ser Lys Thr Gly
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ctgatgagaa atcaggcggt tctgctccaa acgaccattt tatcttcgtg ctctgcaact      2929

tcttcaattc cagagtttct gagaacagac ccaaattcaa tggcatgacc aagaacacct      2989

ggctaccatt ttgttttctc ctgcccttgt tgggtgcatgg ttctaagcat gccctccag      3049

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 <212> PRT
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Ser Trp Glu Gly His Ile Arg Pro Thr Arg Lys Pro Asn Thr Lys Gly
20                      25                      30

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Asn Asn Cys Arg Asp Ser Thr Leu Cys Pro Ala Tyr Ala Thr Cys Thr
35                      40                      45

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Asn Thr Val Asp Ser Tyr Tyr Cys Ala Cys Lys Gln Gly Phe Leu Ser

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- 20 -

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Ser	Asn	Gly	Gln	Asn	His	Phe	Lys	Asp	Pro	Gly	Val	Arg	Cys	Lys	Asp
65					70					75					80
Ile	Asp	Glu	Cys	Ser	Gln	Ser	Pro	Gln	Pro	Cys	Gly	Pro	Asn	Ser	Ser
				85					90					95	
Cys	Lys	Asn	Leu	Ser	Gly	Arg	Tyr	Lys	Cys	Ser	Cys	Leu	Asp	Gly	Phe
			100					105					110		
Ser	Ser	Pro	Thr	Gly	Asn	Asp	Trp	Val	Pro	Gly	Lys	Pro	Gly	Asn	Phe
		115					120					125			
Ser	Cys	Thr	Asp	Ile	Asn	Glu	Cys	Leu	Thr	Ser	Ser	Val	Cys	Pro	Glu
	130					135						140			
His	Ser	Asp	Cys	Val	Asn	Ser	Met	Gly	Ser	Tyr	Ser	Cys	Ser	Cys	Gln
145					150					155					160
Val	Gly	Phe	Ile	Ser	Arg	Asn	Ser	Thr	Cys	Glu	Asp	Val	Asp	Glu	Cys
				165					170					175	
Ala	Asp	Pro	Arg	Ala	Cys	Pro	Glu	His	Ala	Thr	Cys	Asn	Asn	Thr	Val
			180					185					190		
Gly	Asn	Tyr	Ser	Cys	Phe	Cys	Asn	Pro	Gly	Phe	Glu	Ser	Ser	Ser	Gly
		195					200					205			
His	Leu	Ser	Phe	Gln	Gly	Leu	Lys	Ala	Ser	Cys	Glu	Asp	Ile	Asp	Glu
	210					215					220				
Cys	Thr	Glu	Met	Cys	Pro	Ile	Asn	Ser	Thr	Cys	Thr	Asn	Thr	Pro	Gly
225					230					235					240
Ser	Tyr	Phe	Cys	Thr	Cys	His	Pro	Gly	Phe	Ala	Pro	Ser	Asn	Gly	Gln
				245					250					255	
Leu	Asn	Phe	Thr	Asp	Gln	Gly	Val	Glu	Cys	Arg	Asp	Ile	Asp	Glu	Cys
			260					265					270		
Arg	Gln	Asp	Pro	Ser	Thr	Cys	Gly	Pro	Asn	Ser	Ile	Cys	Thr	Asn	Ala
		275					280					285			
Leu	Gly	Ser	Tyr	Ser	Cys	Gly	Cys	Ile	Ala	Gly	Phe	His	Pro	Asn	Pro
	290					295					300				

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Glu Gly Ser Gln Lys Asp Gly Asn Phe Ser Cys Gln Arg Val Leu Phe
 305 310 315 320

Lys Cys Lys Glu Asp Val Ile Pro Asp Asn Lys Gln Ile Gln Gln Cys
 325 330 335

Gln Glu Gly Thr Ala Val Lys Pro Ala Tyr Val Ser Phe Cys Ala Gln
 340 345 350

Ile Asn Asn Ile Phe Ser Val Leu Asp Lys Val Cys Glu Asn Lys Thr
 355 360 365

Thr Val Val Ser Leu Lys Asn Thr Thr Glu Ser Phe Val Pro Val Leu
 370 375 380

Lys Gln Ile Ser Thr Trp Thr Lys Phe Thr Lys Glu Glu Thr Ser Ser
 385 390 395 400

Leu Ala Thr Val Phe Leu Glu Ser Val Glu Ser Met Thr Leu Ala Ser
 405 410 415

Phe Trp Lys Pro Ser Ala Asn Ile Thr Pro Ala Val Arg Thr Glu Tyr
 420 425 430

Leu Asp Ile Glu Ser Lys Val Ile Asn Lys Glu Cys Ser Glu Glu Asn
 435 440 445

Val Thr Leu Asp Leu Val Ala Lys Gly Asp Lys Met Lys Ile Gly Cys
 450 455 460

Ser Thr Ile Glu Glu Ser Glu Ser Thr Glu Thr Thr Gly Val Ala Phe
 465 470 475 480

Val Ser Phe Val Gly Met Glu Ser Val Leu Asn Glu Arg Phe Phe Lys
 485 490 495

Asp His Gln Ala Pro Leu Thr Thr Ser Glu Ile Lys Leu Lys Met Asn
 500 505 510

Ser Arg Val Val Gly Gly Ile Met Thr Gly Glu Lys Lys Asp Gly Phe
 515 520 525

Ser Asp Pro Ile Ile Tyr Thr Leu Glu Asn Ile Gln Pro Lys Gln Lys
 530 535 540

Phe Glu Arg Pro Ile Cys Val Ser Trp Ser Thr Asp Val Lys Gly Gly

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545		550		555		560
Arg Trp Thr Ser Phe Gly Cys Val Ile Leu Glu Ala Ser Glu Thr Tyr						
		565		570		575
Thr Ile Cys Ser Cys Asn Gln Met Ala Asn Leu Ala Val Ile Met Ala						
		580		585		590
Ser Gly Glu Leu Thr Met Asp Phe Ser Leu Tyr Ile Ile Ser His Val						
		595		600		605
Gly Ile Ile Ile Ser Leu Val Cys Leu Val Leu Ala Ile Ala Thr Phe						
		610		615		620
Leu Leu Cys Arg Ser Ile Arg Asn His Asn Thr Tyr Leu His Leu His						
		625		630		635
						640
Leu Cys Val Cys Leu Leu Leu Ala Lys Thr Leu Phe Leu Ala Gly Ile						
		645		650		655
His Lys Thr Asp Asn Lys Met Gly Cys Ala Ile Ile Ala Gly Phe Leu						
		660		665		670
His Tyr Leu Phe Leu Ala Cys Phe Phe Trp Met Leu Val Glu Ala Val						
		675		680		685
Ile Leu Phe Leu Met Val Arg Asn Leu Lys Val Val Asn Tyr Phe Ser						
		690		695		700
Ser Arg Asn Ile Lys Met Leu His Ile Cys Ala Phe Gly Tyr Gly Leu						
		705		710		715
						720
Pro Met Leu Val Val Val Ile Ser Ala Ser Val Gln Pro Gln Gly Tyr						
		725		730		735
Gly Met His Asn Arg Cys Trp Leu Asn Thr Glu Thr Gly Phe Ile Trp						
		740		745		750
Ser Phe Leu Gly Pro Val Cys Thr Val Ile Val Ile Asn Ser Leu Leu						
		755		760		765
Leu Thr Trp Thr Leu Trp Ile Leu Arg Gln Arg Leu Ser Ser Val Asn						
		770		775		780
Ala Glu Val Ser Thr Leu Lys Asp Thr Arg Leu Leu Thr Phe Lys Ala						
		785		790		795
						800

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Phe Ala Gln Leu Phe Ile Leu Gly Cys Ser Trp Val Leu Gly Ile Phe
 805 810 815

Gln Ile Gly Pro Val Ala Gly Val Met Ala Tyr Leu Phe Thr Ile Ile
 820 825 830

Asn Ser Leu Gln Gly Ala Phe Ile Phe Leu Ile His Cys Leu Leu Asn
 835 840 845

Gly Gln Val Arg Glu Glu Tyr Lys Arg Trp Ile Thr Gly Lys Thr Lys
 850 855 860

Pro Ser Ser Gln Ser Gln Thr Ser Arg Ile Leu Leu Ser Ser Met Pro
 865 870 875 880

Ser Ala Ser Lys Thr Gly
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 <213> Homo sapiens

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 aaacgctcac tgggcaaaac accttcactg aaaagagacc tcatattatg caaaaaaaat 180
 cttaaaaggc ctctgccttc agaagttaca ag atg atc aat tca acc tcc aca 233
 Met Ile Asn Ser Thr Ser Thr
 1 5
 cag cct cca gat gaa tcc tgc tct cag aac ctc ctg atc act cag cag 281
 Gln Pro Pro Asp Glu Ser Cys Ser Gln Asn Leu Leu Ile Thr Gln Gln
 10 15 20
 atc att cct gtg ctg tac tgt atg gtc ttc att gca gga atc cta ctc 329
 Ile Ile Pro Val Leu Tyr Cys Met Val Phe Ile Ala Gly Ile Leu Leu
 25 30 35
 aat gga gtg tca gga tgg ata ttc ttt tac gtg ccc agc tct gag agt 377
 Asn Gly Val Ser Gly Trp Ile Phe Phe Tyr Val Pro Ser Ser Glu Ser
 40 45 50 55
 ttc atc atc tat ctc aag aac att gtt att gct gac ttt gtg atg agc 425
 Phe Ile Ile Tyr Leu Lys Asn Ile Val Ile Ala Asp Phe Val Met Ser
 60 65 70

- 24 -

ctg act ttt cct ttc aag atc ctt ggt gac tca ggc ctt ggt ccc tgg	473
Leu Thr Phe Pro Phe Lys Ile Leu Gly Asp Ser Gly Leu Gly Pro Trp	
75 80 85	
cag ctg aac gtg ttt gtg tgc agg gtc tct gcc gtg ctc ttc tac gtc	521
Gln Leu Asn Val Phe Val Cys Arg Val Ser Ala Val Leu Phe Tyr Val	
90 95 100	
aac atg tac gtc agc att gtg ttc ttt ggg ctc atc agc ttt gac aga	569
Asn Met Tyr Val Ser Ile Val Phe Phe Gly Leu Ile Ser Phe Asp Arg	
105 110 115	
tat tat aaa att gta aag cct ctt tgg act tct ttc atc cag tca gtg	617
Tyr Tyr Lys Ile Val Lys Pro Leu Trp Thr Ser Phe Ile Gln Ser Val	
120 125 130 135	
agt tac agc aaa ctt ctg tca gtg ata gta tgg atg ctc atg ctc ctc	665
Ser Tyr Ser Lys Leu Leu Ser Val Ile Val Trp Met Leu Met Leu Leu	
140 145 150	
ctt gct gtt cca aat att att ctc acc aac cag agt gtt agg gag gtt	713
Leu Ala Val Pro Asn Ile Ile Leu Thr Asn Gln Ser Val Arg Glu Val	
155 160 165	
aca caa ata aaa tgt ata gaa ctg aaa agt gaa ctg gga cgg aag tgg	761
Thr Gln Ile Lys Cys Ile Glu Leu Lys Ser Glu Leu Gly Arg Lys Trp	
170 175 180	
cac aaa gca tca aac tac atc ttc gtg gcc atc ttc tgg att gtg ttt	809
His Lys Ala Ser Asn Tyr Ile Phe Val Ala Ile Phe Trp Ile Val Phe	
185 190 195	
ctt ttg tta atc gtt ttc tat act gct atc aca aag aaa atc ttt aag	857
Leu Leu Leu Ile Val Phe Tyr Thr Ala Ile Thr Lys Lys Ile Phe Lys	
200 205 210 215	
tcc cac ctt aag tca agt cgg aat tcc act tcg gtc aaa aag aaa tct	905
Ser His Leu Lys Ser Ser Arg Asn Ser Thr Ser Val Lys Lys Lys Ser	
220 225 230	
agc cgc aac ata ttc agc atc gtg ttt gtg ttt ttt gtc tgt ttt gta	953
Ser Arg Asn Ile Phe Ser Ile Val Phe Val Phe Phe Val Cys Phe Val	
235 240 245	
cct tac cat att gcc aga atc ccc tac aca aag agt cag acc gaa gct	1001
Pro Tyr His Ile Ala Arg Ile Pro Tyr Thr Lys Ser Gln Thr Glu Ala	
250 255 260	
cat tac agc tgc cag tca aaa gaa atc ttg cgg tat atg aaa gaa ttc	1049
His Tyr Ser Cys Gln Ser Lys Glu Ile Leu Arg Tyr Met Lys Glu Phe	
265 270 275	
act ctg cta cta tct gct gca aat gta tgc ttg gac cct att att tat	1097
Thr Leu Leu Leu Ser Ala Ala Asn Val Cys Leu Asp Pro Ile Ile Tyr	
280 285 290 295	
ttc ttt cta tgc cag ccg ttt agg gaa atc tta tgt aag aaa ttg cac	1145
Phe Phe Leu Cys Gln Pro Phe Arg Glu Ile Leu Cys Lys Lys Leu His	
300 305 310	
att cca tta aaa gct cag aat gac cta gac att tcc aga atc aaa aga	1193
Ile Pro Leu Lys Ala Gln Asn Asp Leu Asp Ile Ser Arg Ile Lys Arg	

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315	320	325	
gga aat aca aca ctt gaa agc aca gat act ttg tga gttcctaccc			1239
Gly Asn Thr Thr Leu Glu Ser Thr Asp Thr Leu			
330	335		
tcttccaaag aaagaccacg tgtgcatggt gtcacatctca attacataac agaaatcaat			1299
aagatatgtg ccctcatcat aaatatcatc tctagcactg ccatccaatt tagttcaata			1359
aaattcaaatt ataagtttcc atgctttttt gtaacatcaa agaaaacata cccatcagta			1419
attttctctaa tactgacctt tctattctct attaataaaa aattaatata tacaattatt			1479
caattctatt atattaaaat aagttaaagt ttataaccac tagtctgggc agttaatgta			1539
gaaattttaa tagtaaataa aacacaacat aatcaaagac aactcactca ggcacatcttct			1599
ttctctaaat accagaatct agtatgtaat tgttttcaac actgtcctta aagactaact			1659
tgaaagcagg cacagtttga tgaagggcta gagagctggt tgcaataaaa agtcagggtt			1719
ttttcctgat ttgaagaagc aggaaaagct gacaccaga caatcactta agaaaccct			1779
tattgatgta tttcatggca ctgcaaagga agaggaatat taattgtata cttagcaaga			1839
aaattttttt tttctgatag cactttgagg atattagata catgctaaat atgttttcta			1899
caaagactta cgtcatttaa tgagcctggg gttctgggtg tagaatattt ttaagtaggc			1959
tttactgaga gaaactaaat attggcatac gttatcagca acttcccctg ttcaatagta			2019
tgggaaaaat aagatgactg ggaaaaagac acaccacac cgtagaacat atattaatct			2079
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tctaaaattt acattaatga gtgcaaaata acacataaaa tgaaaattca cacatcacat			2199
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agctaccaaa actaaattct ttctctgcta ttaactggct agaagacatt catctatttt			2319
tcaaagtgtc tttcaaaaca tttttataag taatgtttgt atctatttca tgctttactg			2379
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 <212> PRT
 <213> Homo sapiens

<400> 11

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Asn	Leu	Leu	Ile	Thr	Gln	Gln	Ile	Ile	Pro	Val	Leu	Tyr	Cys	Met	Val
			20				25						30		

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Phe Ile Ala Gly Ile Leu Leu Asn Gly Val Ser Gly Trp Ile Phe Phe
 35 40 45

Tyr Val Pro Ser Ser Glu Ser Phe Ile Ile Tyr Leu Lys Asn Ile Val
 50 55 60

Ile Ala Asp Phe Val Met Ser Leu Thr Phe Pro Phe Lys Ile Leu Gly
 65 70 75 80

Asp Ser Gly Leu Gly Pro Trp Gln Leu Asn Val Phe Val Cys Arg Val
 85 90 95

Ser Ala Val Leu Phe Tyr Val Asn Met Tyr Val Ser Ile Val Phe Phe
 100 105 110

Gly Leu Ile Ser Phe Asp Arg Tyr Tyr Lys Ile Val Lys Pro Leu Trp
 115 120 125

Thr Ser Phe Ile Gln Ser Val Ser Tyr Ser Lys Leu Leu Ser Val Ile
 130 135 140

Val Trp Met Leu Met Leu Leu Leu Ala Val Pro Asn Ile Ile Leu Thr
 145 150 155 160

Asn Gln Ser Val Arg Glu Val Thr Gln Ile Lys Cys Ile Glu Leu Lys
 165 170 175

Ser Glu Leu Gly Arg Lys Trp His Lys Ala Ser Asn Tyr Ile Phe Val
 180 185 190

Ala Ile Phe Trp Ile Val Phe Leu Leu Leu Ile Val Phe Tyr Thr Ala
 195 200 205

Ile Thr Lys Lys Ile Phe Lys Ser His Leu Lys Ser Ser Arg Asn Ser
 210 215 220

Thr Ser Val Lys Lys Lys Ser Ser Arg Asn Ile Phe Ser Ile Val Phe
 225 230 235 240

Val Phe Phe Val Cys Phe Val Pro Tyr His Ile Ala Arg Ile Pro Tyr
 245 250 255

Thr Lys Ser Gln Thr Glu Ala His Tyr Ser Cys Gln Ser Lys Glu Ile
 260 265 270

Leu Arg Tyr Met Lys Glu Phe Thr Leu Leu Leu Ser Ala Ala Asn Val
 275 280 285

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Cys Leu Asp Pro Ile Ile Tyr Phe Phe Leu Cys Gln Pro Phe Arg Glu
 290 295 300

Ile Leu Cys Lys Lys Leu His Ile Pro Leu Lys Ala Gln Asn Asp Leu
 305 310 315 320

Asp Ile Ser Arg Ile Lys Arg Gly Asn Thr Thr Leu Glu Ser Thr Asp
 325 330 335

Thr Leu

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 <213> Homo sapiens

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 tctgcggcgt gactggaggc ccag atg gtc atc atg ggc cag tgc tac tac 111
 Met Val Ile Met Gly Gln Cys Tyr Tyr
 1 5
 aac gag acc atc ggc ttc ttc tat aac aac agt ggc aaa gag ctc agc 159
 Asn Glu Thr Ile Gly Phe Phe Tyr Asn Asn Ser Gly Lys Glu Leu Ser
 10 15 20 25
 tcc cac tgg cgg ccc aag gat gtg gtc gtg gtg gca ctg ggg ctg acc 207
 Ser His Trp Arg Pro Lys Asp Val Val Val Val Ala Leu Gly Leu Thr
 30 35 40
 gtc agc gtg ctg gtg ctg ctg acc aat ctg ctg gtc ata gca gcc atc 255
 Val Ser Val Leu Val Leu Leu Thr Asn Leu Leu Val Ile Ala Ala Ile
 45 50 55
 gcc tcc aac cgc cgc ttc cac cag ccc atc tac tac ctg ctc ggc aat 303
 Ala Ser Asn Arg Arg Phe His Gln Pro Ile Tyr Tyr Leu Leu Gly Asn
 60 65 70
 ctg gcc gcg gct gac ctc ttc gcg ggc gtg gcc tac ctc ttc ctc atg 351
 Leu Ala Ala Ala Asp Leu Phe Ala Gly Val Ala Tyr Leu Phe Leu Met
 75 80 85
 ttc cac act ggt ccc cgc aca gcc cga ctt tca ctt gag ggc tgg ttc 399
 Phe His Thr Gly Pro Arg Thr Ala Arg Leu Ser Leu Glu Gly Trp Phe
 90 95 100 105
 ctg cgg cag ggc ttg ctg gac aca agc ctc act gcg tcg gtg gcc aca 447
 Leu Arg Gln Gly Leu Leu Asp Thr Ser Leu Thr Ala Ser Val Ala Thr
 110 115 120

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ctg ctg gcc atc gcc gtg gag cgg cac cgc agt gtg atg gcc gtg cag Leu Leu Ala Ile Ala Val Glu Arg His Arg Ser Val Met Ala Val Gln 125 130 135	495
ctg cac agc cgc ctg ccc cgt ggc cgc gtg gtc atg ctc att gtg ggc Leu His Ser Arg Leu Pro Arg Gly Arg Val Val Met Leu Ile Val Gly 140 145 150	543
gtg tgg gtg gct gcc ctg ggc ctg ggg ctg ctg cct gcc cac tcc tgg Val Trp Val Ala Ala Leu Gly Leu Gly Leu Leu Pro Ala His Ser Trp 155 160 165	591
cac tgc ctc tgt gcc ctg gac cgc tgc tca cgc atg gca ccc ctg ctc His Cys Leu Cys Ala Leu Asp Arg Cys Ser Arg Met Ala Pro Leu Leu 170 175 180 185	639
agc cgc tcc tat ttg gcc gtc tgg gct ctg tcg agc ctg ctt gtc ttc Ser Arg Ser Tyr Leu Ala Val Trp Ala Leu Ser Ser Leu Leu Val Phe 190 195 200	687
ctg ctc atg gtg gct gtg tac acc cgc att ttc ttc tac gtg cgg cgg Leu Leu Met Val Ala Val Tyr Thr Arg Ile Phe Phe Tyr Val Arg Arg 205 210 215	735
cga gtg cag cgc atg gca gag cat gtc agc tgc cac ccc cgc tac cga Arg Val Gln Arg Met Ala Glu His Val Ser Cys His Pro Arg Tyr Arg 220 225 230	783
gag acc acg ctc agc ctg gtc aag act gtt gtc atc atc ctg ggg gcg Glu Thr Thr Leu Ser Leu Val Lys Thr Val Val Ile Ile Leu Gly Ala 235 240 245	831
ttc gtg gtc tgc tgg aca cca ggc cag gtg gta ctg ctc ctg gat ggt Phe Val Val Cys Trp Thr Pro Gly Gln Val Val Leu Leu Leu Asp Gly 250 255 260 265	879
tta ggc tgt gag tcc tgc aat gtc ctg gct gta gaa aag tac ttc cta Leu Gly Cys Glu Ser Cys Asn Val Leu Ala Val Glu Lys Tyr Phe Leu 270 275 280	927
ctg ttg gcc gag gcc aac tca ctg gtc aat gct gct gtg tac tct tgc Leu Leu Ala Glu Ala Asn Ser Leu Val Asn Ala Ala Val Tyr Ser Cys 285 290 295	975
cga gat gct gag atg cgc cgc acc ttc cgc cgc ctt ctc tgc tgc gcg Arg Asp Ala Glu Met Arg Arg Thr Phe Arg Arg Leu Leu Cys Cys Ala 300 305 310	1023
tgc ctc cgc cag tcc acc cgc gag tct gtc cac tat aca tcc tct gcc Cys Leu Arg Gln Ser Thr Arg Glu Ser Val His Tyr Thr Ser Ser Ala 315 320 325	1071
cag gga ggt gcc agc act cgc atc atg ctt ccc gag aac ggc cac cca Gln Gly Gly Ala Ser Thr Arg Ile Met Leu Pro Glu Asn Gly His Pro 330 335 340 345	1119
ctg atg act cca ccc ttt agc tac ctt gaa ctt cag cgg tac gcg gca Leu Met Thr Pro Pro Phe Ser Tyr Leu Glu Leu Gln Arg Tyr Ala Ala 350 355 360	1167
agc aac aaa tcc aca gcc cct gat gac ttg tgg gtg ctc ctg gct caa	1215

- 29 -

Ser Asn Lys Ser Thr Ala Pro Asp Asp Leu Trp Val Leu Leu Ala Gln
 365 370 375

ccc aac caa cag gac tga ctgactggca ggacaaggctc tggcatggca 1263
 Pro Asn Gln Gln Asp
 380

cagcaccact gccaggcctc cccaggcaca ccactctgcc cagggaatgg gggcttttggg 1323
 tcactctccca ctgcctgggg gagtcagatg ggggtgcagga atctggctct tcagccatct 1383
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 gtttgtggct ccttgcagcc tccagggact ggctgtccc caatagaatt gaagcagtcc 1683
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<400> 13

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Tyr Asn Asn Ser Gly Lys Glu Leu Ser Ser His Trp Arg Pro Lys Asp
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Val Val Val Val Ala Leu Gly Leu Thr Val Ser Val Leu Val Leu Leu
 35 40 45

Thr Asn Leu Leu Val Ile Ala Ala Ile Ala Ser Asn Arg Arg Phe His
 50 55 60

Gln Pro Ile Tyr Tyr Leu Leu Gly Asn Leu Ala Ala Ala Asp Leu Phe
 65 70 75 80

Ala Gly Val Ala Tyr Leu Phe Leu Met Phe His Thr Gly Pro Arg Thr
 85 90 95

Ala Arg Leu Ser Leu Glu Gly Trp Phe Leu Arg Gln Gly Leu Leu Asp
 100 105 110

Thr Ser Leu Thr Ala Ser Val Ala Thr Leu Leu Ala Ile Ala Val Glu
 115 120 125

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Arg His Arg Ser Val Met Ala Val Gln Leu His Ser Arg Leu Pro Arg
 130 135 140

Gly Arg Val Val Met Leu Ile Val Gly Val Trp Val Ala Ala Leu Gly
 145 150 155 160

Leu Gly Leu Leu Pro Ala His Ser Trp His Cys Leu Cys Ala Leu Asp
 165 170 175

Arg Cys Ser Arg Met Ala Pro Leu Leu Ser Arg Ser Tyr Leu Ala Val
 180 185 190

Trp Ala Leu Ser Ser Leu Leu Val Phe Leu Leu Met Val Ala Val Tyr
 195 200 205

Thr Arg Ile Phe Phe Tyr Val Arg Arg Arg Val Gln Arg Met Ala Glu
 210 215 220

His Val Ser Cys His Pro Arg Tyr Arg Glu Thr Thr Leu Ser Leu Val
 225 230 235 240

Lys Thr Val Val Ile Ile Leu Gly Ala Phe Val Val Cys Trp Thr Pro
 245 250 255

Gly Gln Val Val Leu Leu Leu Asp Gly Leu Gly Cys Glu Ser Cys Asn
 260 265 270

Val Leu Ala Val Glu Lys Tyr Phe Leu Leu Leu Ala Glu Ala Asn Ser
 275 280 285

Leu Val Asn Ala Ala Val Tyr Ser Cys Arg Asp Ala Glu Met Arg Arg
 290 295 300

Thr Phe Arg Arg Leu Leu Cys Cys Ala Cys Leu Arg Gln Ser Thr Arg
 305 310 315 320

Glu Ser Val His Tyr Thr Ser Ser Ala Gln Gly Gly Ala Ser Thr Arg
 325 330 335

Ile Met Leu Pro Glu Asn Gly His Pro Leu Met Thr Pro Pro Phe Ser
 340 345 350

Tyr Leu Glu Leu Gln Arg Tyr Ala Ala Ser Asn Lys Ser Thr Ala Pro
 355 360 365

Asp Asp Leu Trp Val Leu Leu Ala Gln Pro Asn Gln Gln Asp

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370 375 380

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 <212> DNA
 <213> Homo sapiens

<220>
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1 5 10 15	
atc ttc ctc act ggc ctc cct gcc aac ctc ctg gcc ctg cgg gcc ttt	96
Ile Phe Leu Thr Gly Leu Pro Ala Asn Leu Leu Ala Leu Arg Ala Phe	
20 25 30	
gtg ggg cgg atc cgc cag ccc cag cct gca cct gtg cac atc ctc ctg	144
Val Gly Arg Ile Arg Gln Pro Gln Pro Ala Pro Val His Ile Leu Leu	
35 40 45	
ctg agc ctg acg ctg gcc gac ctc ctc ctg ctg ctg ctg ctg ccc ttc	192
Leu Ser Leu Thr Leu Ala Asp Leu Leu Leu Leu Leu Leu Leu Pro Phe	
50 55 60	
aag atc atc gag gct gcg tcg aac ttc cgc tgg tac ctg ccc aag gtc	240
Lys Ile Ile Glu Ala Ala Ser Asn Phe Arg Trp Tyr Leu Pro Lys Val	
65 70 75 80	
gtc tgc gcc ctc acg agt ttt ggc ttc tac agc agc atc tac tgc agc	288
Val Cys Ala Leu Thr Ser Phe Gly Phe Tyr Ser Ser Ile Tyr Cys Ser	
85 90 95	
acg tgg ctc ctg gcg ggc atc agc atc gag cgc tac ctg gga gtg gct	336
Thr Trp Leu Leu Ala Gly Ile Ser Ile Glu Arg Tyr Leu Gly Val Ala	
100 105 110	
ttc ccc gtg cag tac aag ctc tcc cgc cgg cct ctg tat gga gtg att	384
Phe Pro Val Gln Tyr Lys Leu Ser Arg Arg Pro Leu Tyr Gly Val Ile	
115 120 125	
gca gct ctg gtg gcc tgg gtt atg tcc ttt ggt cac tgc acc atc gtg	432
Ala Ala Leu Val Ala Trp Val Met Ser Phe Gly His Cys Thr Ile Val	
130 135 140	
atc atc gtt caa tac ttg aac acg act gag cag gtc aga agt ggc aat	480
Ile Ile Val Gln Tyr Leu Asn Thr Thr Glu Gln Val Arg Ser Gly Asn	
145 150 155 160	
gaa att acc tgc tac gag aac ttc acc gat aac cag ttg gac gtg gtg	528
Glu Ile Thr Cys Tyr Glu Asn Phe Thr Asp Asn Gln Leu Asp Val Val	
165 170 175	
ctg ccc gtg cgg ctg gag ctg tgc ctg gtg ctc ttc ttc atc ccc atg	576
Leu Pro Val Arg Leu Glu Leu Cys Leu Val Leu Phe Phe Ile Pro Met	
180 185 190	

- 32 -

gca gtc acc atc ttc tgc tac tgg cgt ttt gtg tgg atc atg ctc tcc 624
 Ala Val Thr Ile Phe Cys Tyr Trp Arg Phe Val Trp Ile Met Leu Ser
 195 200 205

cag ccc ctt gtg ggg gcc cag agg cgg cgc cga gcc gtg ggg ctg gct 672
 Gln Pro Leu Val Gly Ala Gln Arg Arg Arg Arg Ala Val Gly Leu Ala
 210 215 220

gtg gtg acg ctg ctc aat ttc ctg gtg tgc ttc gga cct tac aac gtg 720
 Val Val Thr Leu Leu Asn Phe Leu Val Cys Phe Gly Pro Tyr Asn Val
 225 230 235 240

tcc cac ctg gtg ggg tat cac cag aga aaa agc ccc tgg tgg cgg tca 768
 Ser His Leu Val Gly Tyr His Gln Arg Lys Ser Pro Trp Trp Arg Ser
 245 250 255

ata gcc gtg gtg ttc agt tca ctc aac gcc agt ctg gac ccc ctg ctc 816
 Ile Ala Val Val Phe Ser Ser Leu Asn Ala Ser Leu Asp Pro Leu Leu
 260 265 270

ttc tat ttc tct tct tca gtg gtg cgc agg gca ttt ggg aga ggg ctg 864
 Phe Tyr Phe Ser Ser Ser Val Val Arg Arg Ala Phe Gly Arg Gly Leu
 275 280 285

cag gtg ctg cgg aat cag ggc tcc tcc ctg ttg gga cgc aga ggc aaa 912
 Gln Val Leu Arg Asn Gln Gly Ser Ser Leu Leu Gly Arg Arg Gly Lys
 290 295 300

gac aca gca gag ggg aca aat gag gac agg ggt gtg ggt caa gga gaa 960
 Asp Thr Ala Glu Gly Thr Asn Glu Asp Arg Gly Val Gly Gln Gly Glu
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ggg atg cca agt tgc gac ttc act aca gag tag 993
 Gly Met Pro Ser Ser Asp Phe Thr Thr Glu
 325 330

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 <212> PRT
 <213> Homo sapiens

<400> 15

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Ile Phe Leu Thr Gly Leu Pro Ala Asn Leu Leu Ala Leu Arg Ala Phe
20 25 30

Val Gly Arg Ile Arg Gln Pro Gln Pro Ala Pro Val His Ile Leu Leu
35 40 45

Leu Ser Leu Thr Leu Ala Asp Leu Leu Leu Leu Leu Leu Leu Pro Phe
50 55 60

Lys Ile Ile Glu Ala Ala Ser Asn Phe Arg Trp Tyr Leu Pro Lys Val
65 70 75 80

[illegible]

- 35 -

Arg	Leu	His	Gln	Glu	His	Phe	Pro	Ala	Arg	Leu	Gln	Cys	Val	Val	Asp	
175						180					185					
tac	ggc	ggc	tcc	tcc	agc	acc	gag	aat	gcg	gtg	act	gcc	atc	cgg	ttt	686
Tyr	Gly	Gly	Ser	Ser	Ser	Thr	Glu	Asn	Ala	Val	Thr	Ala	Ile	Arg	Phe	
190					195					200					205	
ctt	ttt	ggc	ttc	ctg	ggg	ccc	ctg	gtg	gcc	gtg	gcc	agc	tgc	cac	agt	734
Leu	Phe	Gly	Phe	Leu	Gly	Pro	Leu	Val	Ala	Val	Ala	Ser	Cys	His	Ser	
				210					215					220		
gcc	ctc	ctg	tgc	tgg	gca	gcc	cga	cgc	tgc	cgg	ccg	ctg	ggc	aca	gcc	782
Ala	Leu	Leu	Cys	Trp	Ala	Ala	Arg	Arg	Cys	Arg	Pro	Leu	Gly	Thr	Ala	
			225				230						235			
att	gtg	gtg	ggg	ttt	ttt	gtc	tgc	tgg	gca	ccc	tac	cac	ctg	ctg	ggg	830
Ile	Val	Val	Gly	Phe	Phe	Val	Cys	Trp	Ala	Pro	Tyr	His	Leu	Leu	Gly	
		240					245					250				
ctg	gtg	ctc	act	gtg	gcg	gcc	ccg	aac	tcc	gca	ctc	ctg	gcc	agg	gcc	878
Leu	Val	Leu	Thr	Val	Ala	Ala	Pro	Asn	Ser	Ala	Leu	Leu	Ala	Arg	Ala	
		255				260					265					
ctg	cgg	gct	gaa	ccc	ctc	atc	gtg	ggc	ctt	gcc	ctc	gct	cac	agc	tgc	926
Leu	Arg	Ala	Glu	Pro	Leu	Ile	Val	Gly	Leu	Ala	Leu	Ala	His	Ser	Cys	
270					275					280					285	
ctc	aat	ccc	atg	ctc	ttc	ctg	tat	ttt	ggg	agg	gct	caa	ctc	cgc	cgg	974
Leu	Asn	Pro	Met	Leu	Phe	Leu	Tyr	Phe	Gly	Arg	Ala	Gln	Leu	Arg	Arg	
				290					295					300		
tca	ctg	cca	gct	gcc	tgt	cac	tgg	gcc	ctg	agg	gag	tcc	cag	ggc	cag	1022
Ser	Leu	Pro	Ala	Ala	Cys	His	Trp	Ala	Leu	Arg	Glu	Ser	Gln	Gly	Gln	
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gac	gaa	agt	gtg	gac	agc	aag	aaa	tcc	acc	agc	cat	gac	ctg	gtc	tcg	1070
Asp	Glu	Ser	Val	Asp	Ser	Lys	Lys	Ser	Thr	Ser	His	Asp	Leu	Val	Ser	
		320					325					330				
gag	atg	gag	gtg	tag	gctggagaga	cattgtgggt	gtgtatcttc	ttatctcatt								1125
Glu	Met	Glu	Val													
		335														
tcacaagact	ggcttcaggc	atagctggat	ccaggagctc	aatgatgtct	tcattttatt											1185
ccttccttca	ttcaacagat	atccatcatg	cacttgctat	gtgcaaggcc	tttttaggca											1245
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 <213> Homo sapiens

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Ser Asp Arg Pro Val Asp Cys Leu Asp Gly Ala Cys Leu Ala Ile Asp

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20	25	30
Pro Leu Arg Val Ala Pro Leu Pro Leu Tyr Ala Ala Ile Phe Leu Val 35 40 45		
Gly Val Pro Gly Asn Ala Met Val Ala Trp Val Ala Gly Lys Val Ala 50 55 60		
Arg Arg Arg Val Gly Ala Thr Trp Leu Leu His Leu Ala Val Ala Asp 65 70 75 80		
Leu Leu Cys Cys Leu Ser Leu Pro Ile Leu Ala Val Pro Ile Ala Arg 85 90 95		
Gly Gly His Trp Pro Tyr Gly Ala Val Gly Cys Arg Ala Leu Pro Ser 100 105 110		
Ile Ile Leu Leu Thr Met Tyr Ala Ser Val Leu Leu Leu Ala Ala Leu 115 120 125		
Ser Ala Asp Leu Cys Phe Leu Ala Leu Gly Pro Ala Trp Trp Ser Thr 130 135 140		
Val Gln Arg Ala Cys Gly Val Gln Val Ala Cys Gly Ala Ala Trp Thr 145 150 155 160		
Leu Ala Leu Leu Leu Thr Val Pro Ser Ala Ile Tyr Arg Arg Leu His 165 170 175		
Gln Glu His Phe Pro Ala Arg Leu Gln Cys Val Val Asp Tyr Gly Gly 180 185 190		
Ser Ser Ser Thr Glu Asn Ala Val Thr Ala Ile Arg Phe Leu Phe Gly 195 200 205		
Phe Leu Gly Pro Leu Val Ala Val Ala Ser Cys His Ser Ala Leu Leu 210 215 220		
Cys Trp Ala Ala Arg Arg Cys Arg Pro Leu Gly Thr Ala Ile Val Val 225 230 235 240		
Gly Phe Phe Val Cys Trp Ala Pro Tyr His Leu Leu Gly Leu Val Leu 245 250 255		
Thr Val Ala Ala Pro Asn Ser Ala Leu Leu Ala Arg Ala Leu Arg Ala 260 265 270		

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Glu Pro Leu Ile Val Gly Leu Ala Leu Ala His Ser Cys Leu Asn Pro
 275 280 285

Met Leu Phe Leu Tyr Phe Gly Arg Ala Gln Leu Arg Arg Ser Leu Pro
 290 295 300

Ala Ala Cys His Trp Ala Leu Arg Glu Ser Gln Gly Gln Asp Glu Ser
 305 310 315 320

Val Asp Ser Lys Lys Ser Thr Ser His Asp Leu Val Ser Glu Met Glu
 325 330 335

Val

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 tgttttcttt tgtttgtata tatgtttatt ggtaacaggt gacactggaa gca atg 176
 Met
 1

aac acc aca gtg atg caa ggc ttc aac aga tct gag cgg tgc ccc aga 224
 Asn Thr Thr Val Met Gln Gly Phe Asn Arg Ser Glu Arg Cys Pro Arg
 5 10 15

gac act cgg ata gta cag ctg gta ttc cca gcc ctc tac aca gtg gtt 272
 Asp Thr Arg Ile Val Gln Leu Val Phe Pro Ala Leu Tyr Thr Val Val
 20 25 30

ttc ttg acc ggc atc ctg ctg aat act ttg gct ctg tgg gtg ttt gtt 320
 Phe Leu Thr Gly Ile Leu Leu Asn Thr Leu Ala Leu Trp Val Phe Val
 35 40 45

cac atc ccc agc tcc tcc acc ttc atc atc tac ctc aaa aac act ttg 368
 His Ile Pro Ser Ser Ser Thr Phe Ile Ile Tyr Leu Lys Asn Thr Leu
 50 55 60 65

gtg gcc gac ttg ata atg aca ctc atg ctt cct ttc aaa atc ctc tct 416
 Val Ala Asp Leu Ile Met Thr Leu Met Leu Pro Phe Lys Ile Leu Ser
 70 75 80

gac tca cac ctg gca ccc tgg cag ctc aga gct ttt gtg tgt cgt ttt 464
 Asp Ser His Leu Ala Pro Trp Gln Leu Arg Ala Phe Val Cys Arg Phe

- 38 -

85	90	95	
tct tcg gtg ata ttt tat gag acc atg tat gtg ggc atc gtg ctg tta			512
Ser Ser Val Ile Phe Tyr Glu Thr Met Tyr Val Gly Ile Val Leu Leu			
100	105	110	
ggg ctc ata gcc ttt gac aga ttc ctc aag atc atc aga cct ttg aga			560
Gly Leu Ile Ala Phe Asp Arg Phe Leu Lys Ile Ile Arg Pro Leu Arg			
115	120	125	
aat att ttt cta aaa aaa cct gtt ttt gca aaa acg gtc tca atc ttc			608
Asn Ile Phe Leu Lys Lys Pro Val Phe Ala Lys Thr Val Ser Ile Phe			
130	135	140	145
atc tgg ttc ttt ttg ttc ttc atc tcc ctg cca aat acg atc ttg agc			656
Ile Trp Phe Phe Leu Phe Phe Ile Ser Leu Pro Asn Thr Ile Leu Ser			
150	155	160	
aac aag gaa gca aca cca tcg tct gtg aaa aag tgt gct tcc tta aag			704
Asn Lys Glu Ala Thr Pro Ser Ser Val Lys Lys Cys Ala Ser Leu Lys			
165	170	175	
ggg cct ctg ggg ctg aaa tgg cat caa atg gta aat aac ata tgc cag			752
Gly Pro Leu Gly Leu Lys Trp His Gln Met Val Asn Asn Ile Cys Gln			
180	185	190	
ttt att ttc tgg act gtt ttt atc cta atg ctt gtg ttt tat gtg gtt			800
Phe Ile Phe Trp Thr Val Phe Ile Leu Met Leu Val Phe Tyr Val Val			
195	200	205	
att gca aaa aaa gta tat gat tct tat aga aag tcc aaa agt aag gac			848
Ile Ala Lys Lys Val Tyr Asp Ser Tyr Arg Lys Ser Lys Ser Lys Asp			
210	215	220	225
aga aaa aac aac aaa aag ctg gaa ggc aaa gta ttt gtt gtc gtg gct			896
Arg Lys Asn Asn Lys Lys Leu Glu Gly Lys Val Phe Val Val Val Ala			
230	235	240	
gtc ttc ttt gtg tgt ttt gct cca ttt cat ttt gcc aga gtt cca tat			944
Val Phe Phe Val Cys Phe Ala Pro Phe His Phe Ala Arg Val Pro Tyr			
245	250	255	
act cac agt caa acc aac aat aag act gac tgt aga ctg caa aat caa			992
Thr His Ser Gln Thr Asn Asn Lys Thr Asp Cys Arg Leu Gln Asn Gln			
260	265	270	
ctg ttt att gct aaa gaa aca act ctc ttt ttg gca gca act aac att			1040
Leu Phe Ile Ala Lys Glu Thr Thr Leu Phe Leu Ala Ala Thr Asn Ile			
275	280	285	
tgt atg gat ccc tta ata tac ata ttc tta tgt aaa aaa ttc aca gaa			1088
Cys Met Asp Pro Leu Ile Tyr Ile Phe Leu Cys Lys Lys Phe Thr Glu			
290	295	300	305
aag cta cca tgt atg caa ggg aga aag acc aca gca tca agc caa gaa			1136
Lys Leu Pro Cys Met Gln Gly Arg Lys Thr Thr Ala Ser Ser Gln Glu			
310	315	320	
aat cat agc agt cag aca gac aac ata acc tta ggc tga caactgtaca			1185
Asn His Ser Ser Gln Thr Asp Asn Ile Thr Leu Gly			
325	330		

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 20 25 30

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 35 40 45

Val His Ile Pro Ser Ser Ser Thr Phe Ile Ile Tyr Leu Lys Asn Thr
 50 55 60

Leu Val Ala Asp Leu Ile Met Thr Leu Met Leu Pro Phe Lys Ile Leu
 65 70 75 80

Ser Asp Ser His Leu Ala Pro Trp Gln Leu Arg Ala Phe Val Cys Arg
 85 90 95

Phe Ser Ser Val Ile Phe Tyr Glu Thr Met Tyr Val Gly Ile Val Leu
 100 105 110

Leu Gly Leu Ile Ala Phe Asp Arg Phe Leu Lys Ile Ile Arg Pro Leu
 115 120 125

Arg Asn Ile Phe Leu Lys Lys Pro Val Phe Ala Lys Thr Val Ser Ile
 130 135 140

Phe Ile Trp Phe Phe Leu Phe Phe Ile Ser Leu Pro Asn Thr Ile Leu
 145 150 155 160

Ser Asn Lys Glu Ala Thr Pro Ser Ser Val Lys Lys Cys Ala Ser Leu
 165 170 175

Lys Gly Pro Leu Gly Leu Lys Trp His Gln Met Val Asn Asn Ile Cys
 180 185 190

Gln Phe Ile Phe Trp Thr Val Phe Ile Leu Met Leu Val Phe Tyr Val
 195 200 205

Val Ile Ala Lys Lys Val Tyr Asp Ser Tyr Arg Lys Ser Lys Ser Lys
 210 215 220

Asp Arg Lys Asn Asn Lys Lys Leu Glu Gly Lys Val Phe Val Val Val
 225 230 235 240

Ala Val Phe Phe Val Cys Phe Ala Pro Phe His Phe Ala Arg Val Pro
245 250 255

Tyr Thr His Ser Gln Thr Asn Asn Lys Thr Asp Cys Arg Leu Gln Asn
260 265 270

Gln Leu Phe Ile Ala Lys Glu Thr Thr Leu Phe Leu Ala Ala Thr Asn
275 280 285

Ile Cys Met Asp Pro Leu Ile Tyr Ile Phe Leu Cys Lys Lys Phe Thr
290 295 300

Glu Lys Leu Pro Cys Met Gln Gly Arg Lys Thr Thr Ala Ser Ser Gln
305 310 315 320

Glu Asn His Ser Ser Gln Thr Asp Asn Ile Thr Leu Gly
325 330

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ggcccaggcc	ctgagaatgg	gttcaaacgg	gccaccacc	ggtaacggta	tcagaaaaaa		840
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                               1                               5

gat aat gca gag ctg ggg tca gcc tct gcc cat ggt acc cca ggc agt      164
Asp Asn Ala Glu Leu Gly Ser Ala Ser Ala His Gly Thr Pro Gly Ser
                               10                               15                               20

gag acg gga cca gaa gag ctg aat act tct gtc tac cac ccc ata aat      212
Glu Thr Gly Pro Glu Glu Leu Asn Thr Ser Val Tyr His Pro Ile Asn
                               25                               30                               35

gga tca cca gat tat cag aaa gca aaa tta caa gtt ctt ggg gcc atc      260
Gly Ser Pro Asp Tyr Gln Lys Ala Lys Leu Gln Val Leu Gly Ala Ile
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cag atc ctg aat gca gca atg att ctg gct ttg ggt gtc ttt ctg ggt      308
Gln Ile Leu Asn Ala Ala Met Ile Leu Ala Leu Gly Val Phe Leu Gly
55                               60                               65                               70

tcc ttg caa tac cca tac cac ttc caa aag cac ttc ttt ttc ttc acc      356
Ser Leu Gln Tyr Pro Tyr His Phe Gln Lys His Phe Phe Phe Phe Thr
                               75                               80                               85

ttc tac aca ggc tac ccg att tgg ggt gct gtg ttt ttc tgt agt tca      404
Phe Tyr Thr Gly Tyr Pro Ile Trp Gly Ala Val Phe Phe Cys Ser Ser
                               90                               95                               100

gga acc ttg tct gtt gta gca ggg ata aaa ccc aca aga aca tgg ata      452
Gly Thr Leu Ser Val Val Ala Gly Ile Lys Pro Thr Arg Thr Trp Ile
                               105                               110                               115

cag aac agt ttt gga atg aac att gcc agt gct aca att gca cta gtg      500
Gln Asn Ser Phe Gly Met Asn Ile Ala Ser Ala Thr Ile Ala Leu Val
120                               125                               130

ggg act gct ttt ctc tca cta aat ata gca gtt aat atc cag tca tta      548
Gly Thr Ala Phe Leu Ser Leu Asn Ile Ala Val Asn Ile Gln Ser Leu
135                               140                               145                               150

agg agt tgt cac tct tca tca gag tca ccg gac cta tgc aat tac atg      596
Arg Ser Cys His Ser Ser Ser Ser Glu Ser Pro Asp Leu Cys Asn Tyr Met
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ggc tcc ata tca aat ggc atg gtg tct cta ctg ctg att ctc acc ttg      644
Gly Ser Ile Ser Asn Gly Met Val Ser Leu Leu Leu Ile Leu Thr Leu
                               170                               175                               180

ctg gaa tta tgc gta act atc tct acc ata gcc atg tgg tgc aat gca      692
Leu Glu Leu Cys Val Thr Ile Ser Thr Ile Ala Met Trp Cys Asn Ala

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185	190	195	
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200	205	210	
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ttaaattctcc agtgactcag agcttcaccc acaaactcag gagaacataa gcctgctcgt			853
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caaattatct aatctctctg atctattttt cctcatctgt aaaatagggtg taataataac			1573
aactactttg tcggttgctc tgagggttaa atgaaaataa aaagaaaatg tgaaacagca			1633
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 <212> PRT
 <213> Homo sapiens

<400> 22

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His	Gly	Thr	Pro	Gly	Ser	Glu	Thr	Gly	Pro	Glu	Glu	Leu	Asn	Thr	Ser
			20					25					30		

Val	Tyr	His	Pro	Ile	Asn	Gly	Ser	Pro	Asp	Tyr	Gln	Lys	Ala	Lys	Leu
		35					40					45			

Gln	Val	Leu	Gly	Ala	Ile	Gln	Ile	Leu	Asn	Ala	Ala	Met	Ile	Leu	Ala
	50					55					60				

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Leu Gly Val Phe Leu Gly Ser Leu Gln Tyr Pro Tyr His Phe Gln Lys
65 70 75 80

His Phe Phe Phe Phe Thr Phe Tyr Thr Gly Tyr Pro Ile Trp Gly Ala
85 90 95

Val Phe Phe Cys Ser Ser Gly Thr Leu Ser Val Val Ala Gly Ile Lys
100 105 110

Pro Thr Arg Thr Trp Ile Gln Asn Ser Phe Gly Met Asn Ile Ala Ser
115 120 125

Ala Thr Ile Ala Leu Val Gly Thr Ala Phe Leu Ser Leu Asn Ile Ala
130 135 140

Val Asn Ile Gln Ser Leu Arg Ser Cys His Ser Ser Ser Glu Ser Pro
145 150 155 160

Asp Leu Cys Asn Tyr Met Gly Ser Ile Ser Asn Gly Met Val Ser Leu
165 170 175

Leu Leu Ile Leu Thr Leu Leu Glu Leu Cys Val Thr Ile Ser Thr Ile
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Ala Met Trp Cys Asn Ala Asn Cys Cys Asn Ser Arg Glu Glu Ile Ser
195 200 205

Ser Pro Pro Asn Ser Val
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<222> (179) .. (1276)

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gcacggcaga gagtctggtg ggggtggaggg gctggcctgg cccctctgtc ctgtggaa 178
atg ctg ggg caa gtg gtc acc ctc ata ctc ctc ctg ctc ctc aag gtg 226
Met Leu Gly Gln Val Val Thr Leu Ile Leu Leu Leu Leu Lys Val
1 5 10 15

tat cag ggc aaa gga tgc cag gga tca gct gac cat gtg gtt agc atc 274

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Tyr	Gln	Gly	Lys	Gly	Cys	Gln	Gly	Ser	Ala	Asp	His	Val	Val	Ser	Ile		
			20					25					30				
tcg	gga	gtg	cct	ctt	cag	tta	caa	cca	aac	agc	ata	cag	acg	aag	gtt	322	
Ser	Gly	Val	Pro	Leu	Gln	Leu	Gln	Pro	Asn	Ser	Ile	Gln	Thr	Lys	Val		
		35					40					45					
gac	agc	att	gca	tgg	aag	aag	ttg	ctg	ccc	tca	caa	aat	gga	ttt	cat	370	
Asp	Ser	Ile	Ala	Trp	Lys	Lys	Leu	Leu	Pro	Ser	Gln	Asn	Gly	Phe	His		
	50					55					60						
cac	ata	ttg	aag	tgg	gag	aat	ggc	tct	ttg	cct	tcc	aat	act	tcc	aat	418	
His	Ile	Leu	Lys	Trp	Glu	Asn	Gly	Ser	Leu	Pro	Ser	Asn	Thr	Ser	Asn		
65					70					75					80		
gat	aga	ttc	agt	ttt	ata	gtc	aag	aac	ttg	agt	ctt	ctc	atc	aag	gca	466	
Asp	Arg	Phe	Ser	Phe	Ile	Val	Lys	Asn	Leu	Ser	Leu	Leu	Ile	Lys	Ala		
				85					90					95			
gct	cag	cag	cag	gac	agt	ggc	ctc	tac	tgc	ctg	gag	gtc	acc	agt	ata	514	
Ala	Gln	Gln	Gln	Asp	Ser	Gly	Leu	Tyr	Cys	Leu	Glu	Val	Thr	Ser	Ile		
			100					105					110				
tct	gga	aaa	gtt	cag	aca	gcc	acg	ttc	cag	gtt	ttt	gta	ttt	gat	aaa	562	
Ser	Gly	Lys	Val	Gln	Thr	Ala	Thr	Phe	Gln	Val	Phe	Val	Phe	Asp	Lys		
		115					120					125					
gtt	gag	aaa	ccc	cgc	cta	cag	ggg	cag	ggg	aag	atc	ctg	gac	aga	ggg	610	
Val	Glu	Lys	Pro	Arg	Leu	Gln	Gly	Gln	Gly	Lys	Ile	Leu	Asp	Arg	Gly		
		130				135					140						
aga	tgc	caa	gtg	gct	ctg	tct	tgc	ttg	gtc	tcc	agg	gat	ggc	aat	gtg	658	
Arg	Cys	Gln	Val	Ala	Leu	Ser	Cys	Leu	Val	Ser	Arg	Asp	Gly	Asn	Val		
145					150					155					160		
tcc	tat	gct	tgg	tac	aga	ggg	agc	aag	ctg	atc	cag	aca	gca	ggg	aac	706	
Ser	Tyr	Ala	Trp	Tyr	Arg	Gly	Ser	Lys	Leu	Ile	Gln	Thr	Ala	Gly	Asn		
				165					170					175			
ctc	acc	tac	ctg	gac	gag	gag	gtt	gac	att	aat	ggc	act	cac	aca	tat	754	
Leu	Thr	Tyr	Leu	Asp	Glu	Glu	Val	Asp	Ile	Asn	Gly	Thr	His	Thr	Tyr		
			180					185					190				
acc	tgc	aat	gtc	agc	aat	cct	gtt	agc	tgg	gaa	agc	cac	acc	ctg	aat	802	
Thr	Cys	Asn	Val	Ser	Asn	Pro	Val	Ser	Trp	Glu	Ser	His	Thr	Leu	Asn		
		195					200					205					
ctc	act	cag	gac	tgt	cag	aat	gcc	cat	cag	gaa	ttc	aga	ttt	tgg	ccg	850	
Leu	Thr	Gln	Asp	Cys	Gln	Asn	Ala	His	Gln	Glu	Phe	Arg	Phe	Trp	Pro		
		210				215					220						
ttt	ttg	gtg	atc	atc	gtg	att	cta	agc	gca	ctg	ttc	ctt	ggc	acc	ctt	898	
Phe	Leu	Val	Ile	Ile	Val	Ile	Leu	Ser	Ala	Leu	Phe	Leu	Gly	Thr	Leu		
225					230					235					240		
gcc	tgc	ttc	tgt	gtg	tgg	agg	aga	aag	agg	aag	gag	aag	cag	tca	gag	946	
Ala	Cys	Phe	Cys	Val	Trp	Arg	Arg	Lys	Arg	Lys	Glu	Lys	Gln	Ser	Glu		
				245					250					255			
acc	agt	ccc	aag	gaa	ttt	ttg	aca	att	tac	gaa	gat	gtc	aag	gat	ctg	994	
Thr	Ser	Pro	Lys	Glu	Phe	Leu	Thr	Ile	Tyr	Glu	Asp	Val	Lys	Asp	Leu		
			260					265					270				

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aaa acc agg aga aat cac gag cag gag cag act ttt cct gga ggg ggg	1042
Lys Thr Arg Arg Asn His Glu Gln Glu Gln Thr Phe Pro Gly Gly Gly	
275 280 285	
agc acc atc tac tct atg atc cag tcc cag tct tct gct ccc acg tca	1090
Ser Thr Ile Tyr Ser Met Ile Gln Ser Gln Ser Ser Ala Pro Thr Ser	
290 295 300	
caa gaa cct gca tat aca tta tat tca tta att cag cct tcc agg aag	1138
Gln Glu Pro Ala Tyr Thr Leu Tyr Ser Leu Ile Gln Pro Ser Arg Lys	
305 310 315 320	
tct gga tcc agg aag agg aac cac agc cct tcc ttc aat agc act atc	1186
Ser Gly Ser Arg Lys Arg Asn His Ser Pro Ser Phe Asn Ser Thr Ile	
325 330 335	
tat gaa gtg att gga aag agt caa cct aaa gcc cag aac cct gct cga	1234
Tyr Glu Val Ile Gly Lys Ser Gln Pro Lys Ala Gln Asn Pro Ala Arg	
340 345 350	
ttg agc cgc aaa gag ctg gag aac ttt gat gtt tat tcc tag	1276
Leu Ser Arg Lys Glu Leu Glu Asn Phe Asp Val Tyr Ser	
355 360 365	
ttgctgcagc aattctcacc tttcttgac atcagcatct gctttgggaa ttggcacagt	1336
ggatgacggc acaggagtct ctatagaaca gttcctagtc tggagaggat atggaaattt	1396
gttcttggtc tatattttgt tttgaaaatg atgtctaaca accatgataa gagcaaggct	1456
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caacaaggct gtggggagca gggctgtgac tctggctgag cccaggaaag cgacaagggt	2296
gaactgggag aggacttact cagagacccc aacagggtgat actgcacaaa gcctgggttct	2356
tcaattttcc taccctgtat ctaacatagg agtttcatat aaaacgggtga tatcatgcag	2416

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atgcagtcctg aattccttgc ctgaattaaa tttatgtatc ctctccaaaa aaaaaaaaaa 2476

aaaaa 2481

<210> 24
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<400> 24

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Tyr Gln Gly Lys Gly Cys Gln Gly Ser Ala Asp His Val Val Ser Ile
 20 25 30

Ser Gly Val Pro Leu Gln Leu Gln Pro Asn Ser Ile Gln Thr Lys Val
 35 40 45

Asp Ser Ile Ala Trp Lys Lys Leu Leu Pro Ser Gln Asn Gly Phe His
 50 55 60

His Ile Leu Lys Trp Glu Asn Gly Ser Leu Pro Ser Asn Thr Ser Asn
 65 70 75 80

Asp Arg Phe Ser Phe Ile Val Lys Asn Leu Ser Leu Leu Ile Lys Ala
 85 90 95

Ala Gln Gln Gln Asp Ser Gly Leu Tyr Cys Leu Glu Val Thr Ser Ile
 100 105 110

Ser Gly Lys Val Gln Thr Ala Thr Phe Gln Val Phe Val Phe Asp Lys
 115 120 125

Val Glu Lys Pro Arg Leu Gln Gly Gln Gly Lys Ile Leu Asp Arg Gly
 130 135 140

Arg Cys Gln Val Ala Leu Ser Cys Leu Val Ser Arg Asp Gly Asn Val
 145 150 155 160

Ser Tyr Ala Trp Tyr Arg Gly Ser Lys Leu Ile Gln Thr Ala Gly Asn
 165 170 175

Leu Thr Tyr Leu Asp Glu Glu Val Asp Ile Asn Gly Thr His Thr Tyr
 180 185 190

Thr Cys Asn Val Ser Asn Pro Val Ser Trp Glu Ser His Thr Leu Asn

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195	200	205
Leu Thr Gln Asp Cys Gln Asn Ala His Gln Glu Phe Arg Phe Trp Pro		
210	215	220
Phe Leu Val Ile Ile Val Ile Leu Ser Ala Leu Phe Leu Gly Thr Leu		
225	230	235 240
Ala Cys Phe Cys Val Trp Arg Arg Lys Arg Lys Glu Lys Gln Ser Glu		
	245	250 255
Thr Ser Pro Lys Glu Phe Leu Thr Ile Tyr Glu Asp Val Lys Asp Leu		
	260	265 270
Lys Thr Arg Arg Asn His Glu Gln Glu Gln Thr Phe Pro Gly Gly Gly		
	275	280 285
Ser Thr Ile Tyr Ser Met Ile Gln Ser Gln Ser Ser Ala Pro Thr Ser		
	290	295 300
Gln Glu Pro Ala Tyr Thr Leu Tyr Ser Leu Ile Gln Pro Ser Arg Lys		
305	310	315 320
Ser Gly Ser Arg Lys Arg Asn His Ser Pro Ser Phe Asn Ser Thr Ile		
	325	330 335
Tyr Glu Val Ile Gly Lys Ser Gln Pro Lys Ala Gln Asn Pro Ala Arg		
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Leu Ser Arg Lys Glu Leu Glu Asn Phe Asp Val Tyr Ser		
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gggggccccg aggccgcagc ttgcctgcgc gctctgagcc ttcgcaactc gcgagcaaag	180
tttggtggag gcaacgccaa gcctgagtcc tttcttcctc tcgttcccca aatccgaggc	240

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agcccgcggg	cgatcatgcc	gcgctcctcc	gcagcctggg	gtacgcgctg	aagcccgggg	300
ggcttggcgc	cggcgaagac	ccaaggacca	ctcttctgcg	tttgaggttg	ctccccacaa	360
ccccgggctc	gtcgctttct	ccatccccgac	ccagccgggg	cgcggggaca	acacaggtcg	420
cggaggagcg	ttgccattca	agtgactgca	gcagcagcgg	cagcgccctcg	gttcctgagc	480
ccaccgcagg	ctgaaggcat	tgcgcgtagt	ccatgcccgt	agaggaagtg	tgcagatggg	540
attaacgtcc	acatggagat	atggaagagg	accggggatt	ggtaccgtaa	cc atg gtc	598
					Met Val	
					1	
agc tgg ggt cgt ttc atc tgc ctg gtc gtg gtc acc atg gca acc ttg	646					
Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val Thr Met Ala Thr Leu						
5 10 15						
tcc ctg gcc cgg ccc tcc ttc agt tta gtt gag gat acc aca tta gag	694					
Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr Leu Glu						
20 25 30						
cca gaa gag cca cca acc aaa tac caa atc tct caa cca gaa gtg tac	742					
Pro Glu Glu Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu Val Tyr						
35 40 45 50						
gtg gct gcg cca ggg gag tcg cta gag gtg cgc tgc ctg ttg aaa gat	790					
Val Ala Ala Pro Gly Glu Ser Leu Glu Val Arg Cys Leu Leu Lys Asp						
55 60 65						
gcc gcc gtg atc agt tgg act aag gat ggg gtg cac ttg ggg ccc aac	838					
Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly Pro Asn						
70 75 80						
aat agg aca gtg ctt att ggg gag tac ttg cag ata aag ggc gcc acg	886					
Asn Arg Thr Val Leu Ile Gly Glu Tyr Leu Gln Ile Lys Gly Ala Thr						
85 90 95						
cct aga gac tcc ggc ctc tat gct tgt act gcc agt agg act gta gac	934					
Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr Val Asp						
100 105 110						
agt gaa act tgg tac ttc atg gtg aat gtc aca gat gcc atc tca tcc	982					
Ser Glu Thr Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile Ser Ser						
115 120 125 130						
gga gat gat gag gat gac acc gat ggt gcg gaa gat ttt gtc agt gag	1030					
Gly Asp Asp Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val Ser Glu						
135 140 145						
aac agt aac aac aag aga gca cca tac tgg acc aac aca gaa aag atg	1078					
Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu Lys Met						
150 155 160						
gaa aag cgg ctc cat gct gtg cct gcg gcc aac act gtc aag ttt cgc	1126					
Glu Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys Phe Arg						
165 170 175						
tgc cca gcc ggg ggg aac cca atg cca acc atg cgg tgg ctg aaa aac	1174					
Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu Lys Asn						
180 185 190						

- 50 -

ggg aag gag ttt aag cag gag cat cgc att gga ggc tac aag gta cga	1222
Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys Val Arg	
195 200 205 210	
aac cag cac tgg agc ctc att atg gaa agt gtg gtc cca tct gac aag	1270
Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser Asp Lys	
215 220 225	
gga aat tat acc tgt gtg gtg gag aat gaa tac ggg tcc atc aat cac	1318
Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile Asn His	
230 235 240	
acg tac cac ctg gat gtt gtg gag cga tcg cct cac cgg ccc atc ctc	1366
Thr Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile Leu	
245 250 255	
caa gcc gga ctg ccg gca aat gcc tcc aca gtg gtc gga gga gac gta	1414
Gln Ala Gly Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly Asp Val	
260 265 270	
gag ttt gtc tgc aag gtt tac agt gat gcc cag ccc cac atc cag tgg	1462
Glu Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp	
275 280 285 290	
atc aag cac gtg gaa aag aac ggc agt aaa tac ggg ccc gac ggg ctg	1510
Ile Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp Gly Leu	
295 300 305	
ccc tac ctc aag gtt ctc aag cac tcg ggg ata aat agt tcc aat gca	1558
Pro Tyr Leu Lys Val Leu Lys His Ser Gly Ile Asn Ser Ser Asn Ala	
310 315 320	
gaa gtg ctg gct ctg ttc aat gtg acc gag gcg gat gct ggg gaa tat	1606
Glu Val Leu Ala Leu Phe Asn Val Thr Glu Ala Asp Ala Gly Glu Tyr	
325 330 335	
ata tgt aag gtc tcc aat tat ata ggg cag gcc aac cag tct gcc tgg	1654
Ile Cys Lys Val Ser Asn Tyr Ile Gly Gln Ala Asn Gln Ser Ala Trp	
340 345 350	
ctc act gtc ctg cca aaa cag caa gcg cct gga aga gaa aag gag att	1702
Leu Thr Val Leu Pro Lys Gln Gln Ala Pro Gly Arg Glu Lys Glu Ile	
355 360 365 370	
aca gct tcc cca gac tac ctg gag ata gcc att tac tgc ata ggg gtc	1750
Thr Ala Ser Pro Asp Tyr Leu Glu Ile Ala Ile Tyr Cys Ile Gly Val	
375 380 385	
ttc tta atc gcc tgt atg gtg gta aca gtc atc ctg tgc cga atg aag	1798
Phe Leu Ile Ala Cys Met Val Val Thr Val Ile Leu Cys Arg Met Lys	
390 395 400	
aac acg acc aag aag cca gac ttc agc agc cag ccg gct gtg cac aag	1846
Asn Thr Thr Lys Lys Pro Asp Phe Ser Ser Gln Pro Ala Val His Lys	
405 410 415	
ctg acc aaa cgt atc ccc ctg cgg aga cag gta aca gtt tcg gct gag	1894
Leu Thr Lys Arg Ile Pro Leu Arg Arg Gln Val Thr Val Ser Ala Glu	
420 425 430	
tcc agc tcc tcc atg aac tcc aac acc ccg ctg gtg agg ata aca aca	1942
Ser Ser Ser Ser Met Asn Ser Asn Thr Pro Leu Val Arg Ile Thr Thr	

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435	440	445	450	
cgc ctc tct tca acg gca gac acc ccc atg ctg gca ggg gtc tcc gag				1990
Arg Leu Ser Ser Thr Ala Asp Thr Pro Met Leu Ala Gly Val Ser Glu				
	455	460	465	
tat gaa ctt cca gag gac cca aaa tgg gag ttt cca aga gat aag ctg				2038
Tyr Glu Leu Pro Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp Lys Leu				
	470	475	480	
aca ctg ggc aag ccc ctg gga gaa ggt tgc ttt ggg caa gtg gtc atg				2086
Thr Leu Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val Met				
	485	490	495	
gcg gaa gca gtg gga att gac aaa gac aag ccc aag gag gcg gtc acc				2134
Ala Glu Ala Val Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala Val Thr				
	500	505	510	
gtg gcc gtg aag atg ttg aaa gat gat gcc aca gag aaa gac ctt tct				2182
Val Ala Val Lys Met Leu Lys Asp Asp Ala Thr Glu Lys Asp Leu Ser				
	515	520	525	530
gat ctg gtg tca gag atg gag atg atg aag atg att ggg aaa cac aag				2230
Asp Leu Val Ser Glu Met Glu Met Met Lys Met Ile Gly Lys His Lys				
	535	540	545	
aat atc ata aat ctt ctt gga gcc tgc aca cag gat ggg cct ctc tat				2278
Asn Ile Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu Tyr				
	550	555	560	
gtc ata gtt gag tat gcc tct aaa ggc aac ctc cga gaa tac ctc cga				2326
Val Ile Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu Arg				
	565	570	575	
gcc cgg agg cca ccc ggg atg gag tac tcc tat gac att aac cgt gtt				2374
Ala Arg Arg Pro Pro Gly Met Glu Tyr Ser Tyr Asp Ile Asn Arg Val				
	580	585	590	
cct gag gag cag atg acc ttc aag gac ttg gtg tca tgc acc tac cag				2422
Pro Glu Glu Gln Met Thr Phe Lys Asp Leu Val Ser Cys Thr Tyr Gln				
	595	600	605	610
ctg gcc aga ggc atg gag tac ttg gct tcc caa aaa tgt att cat cga				2470
Leu Ala Arg Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile His Arg				
	615	620	625	
gat tta gca gcc aga aat gtt ttg gta aca gaa aac aat gtg atg aaa				2518
Asp Leu Ala Ala Arg Asn Val Leu Val Thr Glu Asn Asn Val Met Lys				
	630	635	640	
ata gca gac ttt gga ctc gcc aga gat atc aac aat ata gac tat tac				2566
Ile Ala Asp Phe Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp Tyr Tyr				
	645	650	655	
aaa aag acc acc aat ggg cgg ctt cca gtc aag tgg atg gct cca gaa				2614
Lys Lys Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro Glu				
	660	665	670	
gcc ctg ttt gat aga gta tac act cat cag agt gat gtc tgg tcc ttc				2662
Ala Leu Phe Asp Arg Val Tyr Thr His Gln Ser Asp Val Trp Ser Phe				
	675	680	685	690

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Gly Val Leu Met Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr Pro	
695 700 705	
ggg att ccc gtg gag gaa ctt ttt aag ctg ctg aag gaa gga cac aga	2758
Gly Ile Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His Arg	
710 715 720	
atg gat aag cca gcc aac tgc acc aac gaa ctg tac atg atg atg agg	2806
Met Asp Lys Pro Ala Asn Cys Thr Asn Glu Leu Tyr Met Met Met Arg	
725 730 735	
gac tgt tgg cat gca gtg ccc tcc cag aga cca acg ttc aag cag ttg	2854
Asp Cys Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu	
740 745 750	
gta gaa gac ttg gat cga att ctc act ctc aca acc aat gag gaa tac	2902
Val Glu Asp Leu Asp Arg Ile Leu Thr Leu Thr Thr Asn Glu Glu Tyr	
755 760 765 770	
ttg gac ctc agc caa cct ctc gaa cag tat tca cct agt tac cct gac	2950
Leu Asp Leu Ser Gln Pro Leu Glu Gln Tyr Ser Pro Ser Tyr Pro Asp	
775 780 785	
aca aga agt tct tgt tct tca gga gat gat tct gtt ttt tct cca gac	2998
Thr Arg Ser Ser Cys Ser Ser Gly Asp Asp Ser Val Phe Ser Pro Asp	
790 795 800	
ccc atg cct tac gaa cca tgc ctt cct cag tat cca cac ata aac ggc	3046
Pro Met Pro Tyr Glu Pro Cys Leu Pro Gln Tyr Pro His Ile Asn Gly	
805 810 815	
agt gtt aaa aca tga atgactgtgt ctgcctgtcc ccaaacagga cagcactggg	3101
Ser Val Lys Thr	
820	
aacctagcta cactgagcag ggagaccatg cctcccagag cttgtttgtct ccacttgtat	3161
atatggatca gaggagtaaa taattggaaa agtaatcagc atatgtgtaa agatttatac	3221
agttgaaaac ttgtaatctt ccccaggagg agaagaaggt ttctggagca gtggactgcc	3281
acaagccacc atgtaacccc tctcacctgc cgtgcgtact ggctgtggac cagtaggact	3341
caaggtggac gtgcgtttctg ccttccttgt taatttttgta ataattggag aagatttatg	3401
tcagcacaca cttacagagc acaaatgcag tatataggtg ctggatgtat gtaaataatat	3461
tcaaattatg tataaatata tattatataat ttacaaggag ttatttttttg tattgatttt	3521
aatggatgt cccaatgcac ctagaaaatt ggtctctctt tttttaatag ctatttgcta	3581
aatgctgttc ttacacataa tttcttaatt ttcaccgagc agaggtggaa aaatactttt	3641
gctttcaggg aaaatgggtat aacgttaatt tattaataaa ttggtaatat acaaaacaat	3701
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ctagttaatc tattgcttgg acttaactag ttatcagatc ctttgaaaag agaataattta	3821
caatatatga ctaatttggg gaaaatgaag ttttgattta tttgtgttta aatgctgctg	3881

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tcagacgatt gttcttagac ctctaaatg ccccatatta aaagaactca ttcataaggaa 3941
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ccaagataaa tgggtaccagc gtcctcttaa aagatgcctt aatccattcc ttgaggacag 4061
accttagttg aaatgatagc agaatgtgct tctctctggc agctggcctt ctgcttctga 4121
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tgттаacaag acaaaataaa tgtcacgcaa ctt 4574

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<210> 26
 <211> 822
 <212> PRT
 <213> Homo sapiens

<400> 26

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Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr
          20           25           30

```

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Leu Glu Pro Glu Glu Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu
          35           40           45

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Val Tyr Val Ala Ala Pro Gly Glu Ser Leu Glu Val Arg Cys Leu Leu
50           55           60

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```

Lys Asp Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly
65           70           75           80

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Pro Asn Asn Arg Thr Val Leu Ile Gly Glu Tyr Leu Gln Ile Lys Gly
          85           90           95

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Ala Thr Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr
          100          105          110

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Val Asp Ser Glu Thr Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile
          115          120          125

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Ser Ser Gly Asp Asp Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val
 130 135 140

Ser Glu Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu
 145 150 155 160

Lys Met Glu Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys
 165 170 175

Phe Arg Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu
 180 185 190

Lys Asn Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys
 195 200 205

Val Arg Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser
 210 215 220

Asp Lys Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile
 225 230 235 240

Asn His Thr Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro
 245 250 255

Ile Leu Gln Ala Gly Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly
 260 265 270

Asp Val Glu Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile
 275 280 285

Gln Trp Ile Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp
 290 295 300

Gly Leu Pro Tyr Leu Lys Val Leu Lys His Ser Gly Ile Asn Ser Ser
 305 310 315 320

Asn Ala Glu Val Leu Ala Leu Phe Asn Val Thr Glu Ala Asp Ala Gly
 325 330 335

Glu Tyr Ile Cys Lys Val Ser Asn Tyr Ile Gly Gln Ala Asn Gln Ser
 340 345 350

Ala Trp Leu Thr Val Leu Pro Lys Gln Gln Ala Pro Gly Arg Glu Lys
 355 360 365

- 55 -

Glu Ile Thr Ala Ser Pro Asp Tyr Leu Glu Ile Ala Ile Tyr Cys Ile
 370 375 380

Gly Val Phe Leu Ile Ala Cys Met Val Val Thr Val Ile Leu Cys Arg
 385 390 395 400

Met Lys Asn Thr Thr Lys Lys Pro Asp Phe Ser Ser Gln Pro Ala Val
 405 410 415

His Lys Leu Thr Lys Arg Ile Pro Leu Arg Arg Gln Val Thr Val Ser
 420 425 430

Ala Glu Ser Ser Ser Ser Met Asn Ser Asn Thr Pro Leu Val Arg Ile
 435 440 445

Thr Thr Arg Leu Ser Ser Thr Ala Asp Thr Pro Met Leu Ala Gly Val
 450 455 460

Ser Glu Tyr Glu Leu Pro Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp
 465 470 475 480

Lys Leu Thr Leu Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val
 485 490 495

Val Met Ala Glu Ala Val Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala
 500 505 510

Val Thr Val Ala Val Lys Met Leu Lys Asp Asp Ala Thr Glu Lys Asp
 515 520 525

Leu Ser Asp Leu Val Ser Glu Met Glu Met Met Lys Met Ile Gly Lys
 530 535 540

His Lys Asn Ile Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro
 545 550 555 560

Leu Tyr Val Ile Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr
 565 570 575

Leu Arg Ala Arg Arg Pro Pro Gly Met Glu Tyr Ser Tyr Asp Ile Asn
 580 585 590

Arg Val Pro Glu Glu Gln Met Thr Phe Lys Asp Leu Val Ser Cys Thr
 595 600 605

Tyr Gln Leu Ala Arg Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile
 610 615 620

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His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Thr Glu Asn Asn Val
625 630 635 640

Met Lys Ile Ala Asp Phe Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp
645 650 655

Tyr Tyr Lys Lys Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala
660 665 670

Pro Glu Ala Leu Phe Asp Arg Val Tyr Thr His Gln Ser Asp Val Trp
675 680 685

Ser Phe Gly Val Leu Met Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro
690 695 700

Tyr Pro Gly Ile Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly
705 710 715 720

His Arg Met Asp Lys Pro Ala Asn Cys Thr Asn Glu Leu Tyr Met Met
725 730 735

Met Arg Asp Cys Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys
740 745 750

Gln Leu Val Glu Asp Leu Asp Arg Ile Leu Thr Leu Thr Thr Asn Glu
755 760 765

Glu Tyr Leu Asp Leu Ser Gln Pro Leu Glu Gln Tyr Ser Pro Ser Tyr
770 775 780

Pro Asp Thr Arg Ser Ser Cys Ser Ser Gly Asp Asp Ser Val Phe Ser
785 790 795 800

Pro Asp Pro Met Pro Tyr Glu Pro Cys Leu Pro Gln Tyr Pro His Ile
805 810 815

Asn Gly Ser Val Lys Thr
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<210> 27
<211> 5175
<212> DNA
<213> Homo sapiens

<220>
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<222> (94) .. (2676)

<400> 27

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gggtcgggac actgcctggc agaggctgcg agc atg ggg ccc tgg ggc tgg aaa      114
                Met Gly Pro Trp Gly Trp Lys
                1                      5

ttg cgc tgg acc gtc gcc ttg ctc ctc gcc gcg gcg ggg act gca gtg      162
Leu Arg Trp Thr Val Ala Leu Leu Leu Ala Ala Ala Gly Thr Ala Val
                10                      15                      20

ggc gac aga tgt gaa aga aac gag ttc cag tgc caa gac ggg aaa tgc      210
Gly Asp Arg Cys Glu Arg Asn Glu Phe Gln Cys Gln Asp Gly Lys Cys
                25                      30                      35

atc tcc tac aag tgg gtc tgc gat ggc agc gct gag tgc cag gat ggc      258
Ile Ser Tyr Lys Trp Val Cys Asp Gly Ser Ala Glu Cys Gln Asp Gly
40                      45                      50                      55

tct gat gag tcc cag gag acg tgc ttg tct gtc acc tgc aaa tcc ggg      306
Ser Asp Glu Ser Gln Glu Thr Cys Leu Ser Val Thr Cys Lys Ser Gly
                60                      65                      70

gac ttc agc tgt ggg ggc cgt gtc aac cgc tgc att cct cag ttc tgg      354
Asp Phe Ser Cys Gly Gly Arg Val Asn Arg Cys Ile Pro Gln Phe Trp
                75                      80                      85

agg tgc gat ggc caa gtg gac tgc gac aac ggc tca gac gag caa ggc      402
Arg Cys Asp Gly Gln Val Asp Cys Asp Asn Gly Ser Asp Glu Gln Gly
                90                      95                      100

tgt ccc ccc aag acg tgc tcc cag gac gag ttt cgc tgc cac gat ggg      450
Cys Pro Pro Lys Thr Cys Ser Gln Asp Glu Phe Arg Cys His Asp Gly
                105                      110                      115

aag tgc atc tct cgg cag ttc gtc tgt gac tca gac cgg gac tgc ttg      498
Lys Cys Ile Ser Arg Gln Phe Val Cys Asp Ser Asp Arg Asp Cys Leu
120                      125                      130                      135

gac ggc tca gac gag gcc tcc tgc ccg gtg ctc acc tgt ggt ccc gcc      546
Asp Gly Ser Asp Glu Ala Ser Cys Pro Val Leu Thr Cys Gly Pro Ala
                140                      145                      150

agc ttc cag tgc aac agc tcc acc tgc atc ccc cag ctg tgg gcc tgc      594
Ser Phe Gln Cys Asn Ser Ser Thr Cys Ile Pro Gln Leu Trp Ala Cys
                155                      160                      165

gac aac gac ccc gac tgc gaa gat ggc tcg gat gag tgg ccg cag cgc      642
Asp Asn Asp Pro Asp Cys Glu Asp Gly Ser Asp Glu Trp Pro Gln Arg
                170                      175                      180

tgt agg ggt ctt tac gtg ttc caa ggg gac agt agc ccc tgc tcg gcc      690
Cys Arg Gly Leu Tyr Val Phe Gln Gly Asp Ser Ser Pro Cys Ser Ala
                185                      190                      195

ttc gag ttc cac tgc cta agt ggc gag tgc atc cac tcc agc tgg cgc      738
Phe Glu Phe His Cys Leu Ser Gly Glu Cys Ile His Ser Ser Trp Arg
200                      205                      210                      215

tgt gat ggt ggc ccc gac tgc aag gac aaa tct gac gag gaa aac tgc      786

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Cys	Asp	Gly	Gly	Pro	Asp	Cys	Lys	Asp	Lys	Ser	Asp	Glu	Glu	Asn	Cys	
				220					225					230		
gct	gtg	gcc	acc	tgt	cgc	cct	gac	gaa	ttc	cag	tgc	tct	gat	gga	aac	834
Ala	Val	Ala	Thr	Cys	Arg	Pro	Asp	Glu	Phe	Gln	Cys	Ser	Asp	Gly	Asn	
			235					240					245			
tgc	atc	cat	ggc	agc	cgg	cag	tgt	gac	cgg	gaa	tat	gac	tgc	aag	gac	882
Cys	Ile	His	Gly	Ser	Arg	Gln	Cys	Asp	Arg	Glu	Tyr	Asp	Cys	Lys	Asp	
		250					255					260				
atg	agc	gat	gaa	gtt	ggc	tgc	gtt	aat	gtg	aca	ctc	tgc	gag	gga	ccc	930
Met	Ser	Asp	Glu	Val	Gly	Cys	Val	Asn	Val	Thr	Leu	Cys	Glu	Gly	Pro	
	265					270					275					
aac	aag	ttc	aag	tgt	cac	agc	ggc	gaa	tgc	atc	acc	ctg	gac	aaa	gtc	978
Asn	Lys	Phe	Lys	Cys	His	Ser	Gly	Glu	Cys	Ile	Thr	Leu	Asp	Lys	Val	
280					285					290					295	
tgc	aac	atg	gct	aga	gac	tgc	cgg	gac	tgg	tca	gat	gaa	ccc	atc	aaa	1026
Cys	Asn	Met	Ala	Arg	Asp	Cys	Arg	Asp	Trp	Ser	Asp	Glu	Pro	Ile	Lys	
				300					305					310		
gag	tgc	ggg	acc	aac	gaa	tgc	ttg	gac	aac	aac	ggc	ggc	tgt	tcc	cac	1074
Glu	Cys	Gly	Thr	Asn	Glu	Cys	Leu	Asp	Asn	Asn	Gly	Gly	Cys	Ser	His	
			315					320					325			
gtc	tgc	aat	gac	ctt	aag	atc	ggc	tac	gag	tgc	ctg	tgc	ccc	gac	ggc	1122
Val	Cys	Asn	Asp	Leu	Lys	Ile	Gly	Tyr	Glu	Cys	Leu	Cys	Pro	Asp	Gly	
		330					335					340				
ttc	cag	ctg	gtg	gcc	cag	cga	aga	tgc	gaa	gat	atc	gat	gag	tgt	cag	1170
Phe	Gln	Leu	Val	Ala	Gln	Arg	Arg	Cys	Glu	Asp	Ile	Asp	Glu	Cys	Gln	
	345					350					355					
gat	ccc	gac	acc	tgc	agc	cag	ctc	tgc	gtg	aac	ctg	gag	ggc	ggc	tac	1218
Asp	Pro	Asp	Thr	Cys	Ser	Gln	Leu	Cys	Val	Asn	Leu	Glu	Gly	Gly	Tyr	
360					365					370					375	
aag	tgc	cag	tgt	gag	gaa	ggc	ttc	cag	ctg	gac	ccc	cac	acg	aag	gcc	1266
Lys	Cys	Gln	Cys	Glu	Glu	Gly	Phe	Gln	Leu	Asp	Pro	His	Thr	Lys	Ala	
				380					385					390		
tgc	aag	gct	gtg	ggc	tcc	atc	gcc	tac	ctc	ttc	ttc	acc	aac	cgg	cac	1314
Cys	Lys	Ala	Val	Gly	Ser	Ile	Ala	Tyr	Leu	Phe	Phe	Thr	Asn	Arg	His	
			395					400					405			
gag	gtc	agg	aag	atg	acg	ctg	gac	cgg	agc	gag	tac	acc	agc	ctc	atc	1362
Glu	Val	Arg	Lys	Met	Thr	Leu	Asp	Arg	Ser	Glu	Tyr	Thr	Ser	Leu	Ile	
		410					415					420				
ccc	aac	ctg	agg	aac	gtg	gtc	gct	ctg	gac	acg	gag	gtg	gcc	agc	aat	1410
Pro	Asn	Leu	Arg	Asn	Val	Val	Ala	Leu	Asp	Thr	Glu	Val	Ala	Ser	Asn	
	425					430						435				
aga	atc	tac	tgg	tct	gac	ctg	tcc	cag	aga	atg	atc	tgc	agc	acc	cag	1458
Arg	Ile	Tyr	Trp	Ser	Asp	Leu	Ser	Gln	Arg	Met	Ile	Cys	Ser	Thr	Gln	
440					445					450					455	
ctt	gac	aga	gcc	cac	ggc	gtc	tct	tcc	tat	gac	acc	gtc	atc	agc	agg	1506
Leu	Asp	Arg	Ala	His	Gly	Val	Ser	Ser	Tyr	Asp	Thr	Val	Ile	Ser	Arg	
				460					465						470	

- 59 -

gac atc cag gcc ccc gac ggg ctg gct gtg gac tgg atc cac agc aac	1554
Asp Ile Gln Ala Pro Asp Gly Leu Ala Val Asp Trp Ile His Ser Asn	
475 480 485	
atc tac tgg acc gac tct gtc ctg ggc act gtc tct gtt gcg gat acc	1602
Ile Tyr Trp Thr Asp Ser Val Leu Gly Thr Val Ser Val Ala Asp Thr	
490 495 500	
aag ggc gtg aag agg aaa acg tta ttc agg gag aac ggc tcc aag cca	1650
Lys Gly Val Lys Arg Lys Thr Leu Phe Arg Glu Asn Gly Ser Lys Pro	
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agg gcc atc gtg gtg gat cct gtt cat ggc ttc atg tac tgg act gac	1698
Arg Ala Ile Val Val Asp Pro Val His Gly Phe Met Tyr Trp Thr Asp	
520 525 530 535	
tgg gga act ccc gcc aag atc aag aaa ggg ggc ctg aat ggt gtg gac	1746
Trp Gly Thr Pro Ala Lys Ile Lys Lys Gly Gly Leu Asn Gly Val Asp	
540 545 550	
atc tac tcg ctg gtg act gaa aac att cag tgg ccc aat ggc atc acc	1794
Ile Tyr Ser Leu Val Thr Glu Asn Ile Gln Trp Pro Asn Gly Ile Thr	
555 560 565	
cta gat ctc ctc agt ggc cgc ctc tac tgg gtt gac tcc aaa ctt cac	1842
Leu Asp Leu Leu Ser Gly Arg Leu Tyr Trp Val Asp Ser Lys Leu His	
570 575 580	
tcc atc tca agc atc gat gtc aat ggg ggc aac cgg aag acc atc ttg	1890
Ser Ile Ser Ser Ile Asp Val Asn Gly Gly Asn Arg Lys Thr Ile Leu	
585 590 595	
gag gat gaa aag agg ctg gcc cac ccc ttc tcc ttg gcc gtc ttt gag	1938
Glu Asp Glu Lys Arg Leu Ala His Pro Phe Ser Leu Ala Val Phe Glu	
600 605 610 615	
gac aaa gta ttt tgg aca gat atc atc aac gaa gcc att ttc agt gcc	1986
Asp Lys Val Phe Trp Thr Asp Ile Ile Asn Glu Ala Ile Phe Ser Ala	
620 625 630	
aac cgc ctc aca ggt tcc gat gtc aac ttg ttg gct gaa aac cta ctg	2034
Asn Arg Leu Thr Gly Ser Asp Val Asn Leu Leu Ala Glu Asn Leu Leu	
635 640 645	
tcc cca gag gat atg gtc ctc ttc cac aac ctc acc cag cca aga gga	2082
Ser Pro Glu Asp Met Val Leu Phe His Asn Leu Thr Gln Pro Arg Gly	
650 655 660	
gtg aac tgg tgt gag agg acc acc ctg agc aat ggc ggc tgc cag tat	2130
Val Asn Trp Cys Glu Arg Thr Thr Leu Ser Asn Gly Gly Cys Gln Tyr	
665 670 675	
ctg tgc ctc cct gcc ccg cag atc aac ccc cac tcg ccc aag ttt acc	2178
Leu Cys Leu Pro Ala Pro Gln Ile Asn Pro His Ser Pro Lys Phe Thr	
680 685 690 695	
tgc gcc tgc ccg gac ggc atg ctg ctg gcc agg gac atg agg agc tgc	2226
Cys Ala Cys Pro Asp Gly Met Leu Leu Ala Arg Asp Met Arg Ser Cys	
700 705 710	
ctc aca gag gct gag gct gca gtg gcc acc cag gag aca tcc acc gtc	2274

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caggacacca	gcctggtgcc	catcctcccg	acccctaccc	acttccattc	ccgtggtctc	3486
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tcttaaatg						5175

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<210> 28
 <211> 860
 <212> PRT
 <213> Homo sapiens

<400> 28

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Ala Ala Ala Gly Thr Ala Val Gly Asp Arg Cys Glu Arg Asn Glu Phe
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Gln Cys Gln Asp Gly Lys Cys Ile Ser Tyr Lys Trp Val Cys Asp Gly
 35 40 45

Ser Ala Glu Cys Gln Asp Gly Ser Asp Glu Ser Gln Glu Thr Cys Leu
 50 55 60

Ser Val Thr Cys Lys Ser Gly Asp Phe Ser Cys Gly Gly Arg Val Asn
 65 70 75 80

Arg Cys Ile Pro Gln Phe Trp Arg Cys Asp Gly Gln Val Asp Cys Asp
 85 90 95

Asn Gly Ser Asp Glu Gln Gly Cys Pro Pro Lys Thr Cys Ser Gln Asp
 100 105 110

Glu Phe Arg Cys His Asp Gly Lys Cys Ile Ser Arg Gln Phe Val Cys
 115 120 125

Asp Ser Asp Arg Asp Cys Leu Asp Gly Ser Asp Glu Ala Ser Cys Pro
 130 135 140

Val Leu Thr Cys Gly Pro Ala Ser Phe Gln Cys Asn Ser Ser Thr Cys
 145 150 155 160

Ile Pro Gln Leu Trp Ala Cys Asp Asn Asp Pro Asp Cys Glu Asp Gly
 165 170 175

Ser Asp Glu Trp Pro Gln Arg Cys Arg Gly Leu Tyr Val Phe Gln Gly
 180 185 190

Asp Ser Ser Pro Cys Ser Ala Phe Glu Phe His Cys Leu Ser Gly Glu
 195 200 205

Cys Ile His Ser Ser Trp Arg Cys Asp Gly Gly Pro Asp Cys Lys Asp
 210 215 220

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Lys Ser Asp Glu Glu Asn Cys Ala Val Ala Thr Cys Arg Pro Asp Glu
 225 230 235 240

Phe Gln Cys Ser Asp Gly Asn Cys Ile His Gly Ser Arg Gln Cys Asp
 245 250 255

Arg Glu Tyr Asp Cys Lys Asp Met Ser Asp Glu Val Gly Cys Val Asn
 260 265 270

Val Thr Leu Cys Glu Gly Pro Asn Lys Phe Lys Cys His Ser Gly Glu
 275 280 285

Cys Ile Thr Leu Asp Lys Val Cys Asn Met Ala Arg Asp Cys Arg Asp
 290 295 300

Trp Ser Asp Glu Pro Ile Lys Glu Cys Gly Thr Asn Glu Cys Leu Asp
 305 310 315 320

Asn Asn Gly Gly Cys Ser His Val Cys Asn Asp Leu Lys Ile Gly Tyr
 325 330 335

Glu Cys Leu Cys Pro Asp Gly Phe Gln Leu Val Ala Gln Arg Arg Cys
 340 345 350

Glu Asp Ile Asp Glu Cys Gln Asp Pro Asp Thr Cys Ser Gln Leu Cys
 355 360 365

Val Asn Leu Glu Gly Gly Tyr Lys Cys Gln Cys Glu Glu Gly Phe Gln
 370 375 380

Leu Asp Pro His Thr Lys Ala Cys Lys Ala Val Gly Ser Ile Ala Tyr
 385 390 395 400

Leu Phe Phe Thr Asn Arg His Glu Val Arg Lys Met Thr Leu Asp Arg
 405 410 415

Ser Glu Tyr Thr Ser Leu Ile Pro Asn Leu Arg Asn Val Val Ala Leu
 420 425 430

Asp Thr Glu Val Ala Ser Asn Arg Ile Tyr Trp Ser Asp Leu Ser Gln
 435 440 445

Arg Met Ile Cys Ser Thr Gln Leu Asp Arg Ala His Gly Val Ser Ser
 450 455 460

Tyr Asp Thr Val Ile Ser Arg Asp Ile Gln Ala Pro Asp Gly Leu Ala

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465		470		475		480
Val Asp Trp Ile His Ser Asn Ile Tyr Trp Thr Asp Ser Val Leu Gly						
	485			490		495
Thr Val Ser Val Ala Asp Thr Lys Gly Val Lys Arg Lys Thr Leu Phe						
	500			505		510
Arg Glu Asn Gly Ser Lys Pro Arg Ala Ile Val Val Asp Pro Val His						
	515			520		525
Gly Phe Met Tyr Trp Thr Asp Trp Gly Thr Pro Ala Lys Ile Lys Lys						
	530			535		540
Gly Gly Leu Asn Gly Val Asp Ile Tyr Ser Leu Val Thr Glu Asn Ile						
	545			550		555
Gln Trp Pro Asn Gly Ile Thr Leu Asp Leu Leu Ser Gly Arg Leu Tyr						
	565			570		575
Trp Val Asp Ser Lys Leu His Ser Ile Ser Ser Ile Asp Val Asn Gly						
	580			585		590
Gly Asn Arg Lys Thr Ile Leu Glu Asp Glu Lys Arg Leu Ala His Pro						
	595			600		605
Phe Ser Leu Ala Val Phe Glu Asp Lys Val Phe Trp Thr Asp Ile Ile						
	610			615		620
Asn Glu Ala Ile Phe Ser Ala Asn Arg Leu Thr Gly Ser Asp Val Asn						
	625			630		635
Leu Leu Ala Glu Asn Leu Leu Ser Pro Glu Asp Met Val Leu Phe His						
	645			650		655
Asn Leu Thr Gln Pro Arg Gly Val Asn Trp Cys Glu Arg Thr Thr Leu						
	660			665		670
Ser Asn Gly Gly Cys Gln Tyr Leu Cys Leu Pro Ala Pro Gln Ile Asn						
	675			680		685
Pro His Ser Pro Lys Phe Thr Cys Ala Cys Pro Asp Gly Met Leu Leu						
	690			695		700
Ala Arg Asp Met Arg Ser Cys Leu Thr Glu Ala Glu Ala Ala Val Ala						
	705			710		715
						720

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Thr Gln Glu Thr Ser Thr Val Arg Leu Lys Val Ser Ser Thr Ala Val
 725 730 735

Arg Thr Gln His Thr Thr Thr Arg Pro Val Pro Asp Thr Ser Arg Leu
 740 745 750

Pro Gly Ala Thr Pro Gly Leu Thr Thr Val Glu Ile Val Thr Met Ser
 755 760 765

His Gln Ala Leu Gly Asp Val Ala Gly Arg Gly Asn Glu Lys Lys Pro
 770 775 780

Ser Ser Val Arg Ala Leu Ser Ile Val Leu Pro Ile Val Leu Leu Val
 785 790 795 800

Phe Leu Cys Leu Gly Val Phe Leu Leu Trp Lys Asn Trp Arg Leu Lys
 805 810 815

Asn Ile Asn Ser Ile Asn Phe Asp Asn Pro Val Tyr Gln Lys Thr Thr
 820 825 830

Glu Asp Glu Val His Ile Cys His Asn Gln Asp Gly Tyr Ser Tyr Pro
 835 840 845

Ser Arg Gln Met Val Ser Leu Glu Asp Asp Val Ala
 850 855 860

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 <211> 2070
 <212> DNA
 <213> Homo sapiens

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 tcatctgttt tcatagtgtg agatcaaccc acaggaatat ccatggcttt tgtgctcatt 180
 ttggttctca gtttctacga gctggtgtca ggacagtggc aagtcactgg accgggcaag 240
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 tacagagatg gggaagactg ggaatctaag cagatgccac agtatcgagg gagaactgag 420
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 tgggagctgc ggggtggcagc actgggctca cttcctctca tttccatcgt gggatatgtt 600

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gacggaggta tccagttact ctgcctgtcc tcaggctggg tccccagcc cacagccaag    660
tggaagggtc cacaaggaca ggatttgtct tcagactcca gagcaaatgc agatgggtac    720
agcctgtatg atgtggagat ctccattata gtccaggaaa atgctgggag catattgtgt    780
tccatccacc ttgctgagca gagtcatgag gtggaatcca aggtattgat aggagagacg    840
tttttccagc cctcaccttg gcgcctggct tctattttac tcgggttact ctgtgggtgcc    900
ctgtgtgggtg ttgtcatggg gatgataatt gttttcttca aatccaaagg gaaaatccag    960
gcggaactgg actggagaag aaagcacgga caggcagaat tgagagacgc ccggaaacac   1020
gcagtggagg tgactctgga tccagagacg gctcacccga agctctgcgt ttctgatctg   1080
aaaactgtaa cccatagaaa agctccccag gaggtgcctc actctgagaa gagatttaca   1140
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gtgggacaaa atgtagggtg gtatgtggga gtgtgtcggg atgacgtaga cagggggaag   1260
aacaatgtga ctttgtctcc caacaatggg tattgggtcc tcagactgac aacagaacat   1320
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catgcatgt atgacgagga aaaggggact cccatattca tatgtccagt gtcctgggga   1560
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ccctgaagtg gggacggaat agactcacat taggtttagt ttgtgaaaac tccatccagc   1860
taagcgatct tgaacaagtc acaacctccc aggctcctca tttgctagtc acggacagtg   1920
attcctgcct cacagggtgaa gattaaagag acaacgaatg tgaatcatgc ttgcaggttt   1980
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 <212> DNA
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cagagcaggg cagtgggagg agacgcc atg acc ccc atc ctc acg gtc ctg atc      114
               Met Thr Pro Ile Leu Thr Val Leu Ile
                   1                   5

tgt ctc ggg ctg agt ctg ggc ccc agg acc cac gtg cag gca ggg cac      162
Cys Leu Gly Leu Ser Leu Gly Pro Arg Thr His Val Gln Ala Gly His
10                   15                   20                   25

ctc ccc aag ccc acc ctc tgg gct gag cca ggc tct gtg atc atc cag      210
Leu Pro Lys Pro Thr Leu Trp Ala Glu Pro Gly Ser Val Ile Ile Gln
                   30                   35                   40

gga agt cct gtg acc ctc agg tgt cag ggg agc ctt cag gct gag gag      258
Gly Ser Pro Val Thr Leu Arg Cys Gln Gly Ser Leu Gln Ala Glu Glu
                   45                   50                   55

tac cat cta tat agg gaa aac aaa tca gca tcc tgg gtt aga cgg ata      306
Tyr His Leu Tyr Arg Glu Asn Lys Ser Ala Ser Trp Val Arg Arg Ile
                   60                   65                   70

caa gag cct ggg aag aat ggc cag ttc ccc atc cca tcc atc acc tgg      354
Gln Glu Pro Gly Lys Asn Gly Gln Phe Pro Ile Pro Ser Ile Thr Trp
                   75                   80                   85

gaa cac gca ggg cgg tat cac tgt cag tac tac agc cac aat cac tca      402
Glu His Ala Gly Arg Tyr His Cys Gln Tyr Tyr Ser His Asn His Ser
90                   95                   100                   105

tca gag tac agt gac ccc ctg gag ctg gtg gtg aca gga gcc tac agc      450
Ser Glu Tyr Ser Asp Pro Leu Glu Leu Val Val Thr Gly Ala Tyr Ser
                   110                   115                   120

aaa ccc acc ctc tca gct ctg ccc agc cct gtg gtg acc tta gga ggg      498
Lys Pro Thr Leu Ser Ala Leu Pro Ser Pro Val Val Thr Leu Gly Gly
                   125                   130                   135

aac gtg acc ctc cag tgt gtc tca cag gtg gca ttt gac ggc ttc att      546
Asn Val Thr Leu Gln Cys Val Ser Gln Val Ala Phe Asp Gly Phe Ile
                   140                   145                   150

ctg tgt aag gaa gga gaa gat gaa cac cca caa cgc ctg aac tcc cat      594
Leu Cys Lys Glu Gly Glu Asp Glu His Pro Gln Arg Leu Asn Ser His
                   155                   160                   165

tcc cat gcc cgt ggg tgg tcc tgg gcc atc ttc tcc gtg ggc ccc gtg      642
Ser His Ala Arg Gly Trp Ser Trp Ala Ile Phe Ser Val Gly Pro Val
170                   175                   180                   185

agc ccg agt cgc agg tgg tcg tac agg tgc tat gct tat gac tcg aac      690
Ser Pro Ser Arg Arg Trp Ser Tyr Arg Cys Tyr Ala Tyr Asp Ser Asn
                   190                   195                   200

tct ccc tat gtg tgg tct cta ccc agt gat ctc ctg gag ctc ctg gtc      738
Ser Pro Tyr Val Trp Ser Leu Pro Ser Asp Leu Leu Glu Leu Leu Val
                   205                   210                   215

cca ggt gtt tct aag aag cca tca ctc tca gtg cag cca ggt cct atg      786
Pro Gly Val Ser Lys Lys Pro Ser Leu Ser Val Gln Pro Gly Pro Met
                   220                   225                   230

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gtg gcc cct ggg gag agc ctg acc ctc cag tgt gtc tct gat gtc ggc	834
Val Ala Pro Gly Glu Ser Leu Thr Leu Gln Cys Val Ser Asp Val Gly	
235 240 245	
tac gac aga ttt gtt ctg tat aag gag gga gaa cgt gac ttc ctc cag	882
Tyr Asp Arg Phe Val Leu Tyr Lys Glu Gly Glu Arg Asp Phe Leu Gln	
250 255 260 265	
cgc cct ggt tgg cag ccc cag gct ggg ctc tcc cag gcc aac ttc acc	930
Arg Pro Gly Trp Gln Pro Gln Ala Gly Leu Ser Gln Ala Asn Phe Thr	
270 275 280	
ctg ggc cct gtg agc ccc tcc cac ggg ggc cag tac aga tgc tac agt	978
Leu Gly Pro Val Ser Pro Ser His Gly Gly Gln Tyr Arg Cys Tyr Ser	
285 290 295	
gca cac aac ctc tcc tcc gag tgg tcg gcc ccc agt gac ccc ctg gac	1026
Ala His Asn Leu Ser Ser Glu Trp Ser Ala Pro Ser Asp Pro Leu Asp	
300 305 310	
atc ctg atc aca gga cag ttc tat gac aga ccc tct ctc tcg gtg cag	1074
Ile Leu Ile Thr Gly Gln Phe Tyr Asp Arg Pro Ser Leu Ser Val Gln	
315 320 325	
ccg gtc ccc aca gta gcc cca gga aag aac gtg acc ctg ctg tgt cag	1122
Pro Val Pro Thr Val Ala Pro Gly Lys Asn Val Thr Leu Leu Cys Gln	
330 335 340 345	
tca cgg ggg cag ttc cac act ttc ctt ctg acc aag gag ggg gca ggc	1170
Ser Arg Gly Gln Phe His Thr Phe Leu Leu Thr Lys Glu Gly Ala Gly	
350 355 360	
cat ccc cca ctg cat ctg aga tca gag cac caa gct cag cag aac cag	1218
His Pro Pro Leu His Leu Arg Ser Glu His Gln Ala Gln Gln Asn Gln	
365 370 375	
gct gaa ttc cgc atg ggt cct gtg acc tca gcc cac gtg ggg acc tac	1266
Ala Glu Phe Arg Met Gly Pro Val Thr Ser Ala His Val Gly Thr Tyr	
380 385 390	
aga tgc tac agc tca ctc agc tcc aac ccc tac ctg ctg tct ctc ccc	1314
Arg Cys Tyr Ser Ser Leu Ser Ser Asn Pro Tyr Leu Leu Ser Leu Pro	
395 400 405	
agt gac ccc ctg gag ctc gtg gtc tca gca tcc cta ggc caa cac ccc	1362
Ser Asp Pro Leu Glu Leu Val Val Ser Ala Ser Leu Gly Gln His Pro	
410 415 420 425	
cag gat tac aca gtg gag aat ctc atc cgc atg ggt gtg gct ggc ttg	1410
Gln Asp Tyr Thr Val Glu Asn Leu Ile Arg Met Gly Val Ala Gly Leu	
430 435 440	
gtc ctg gtg gtc ctc ggg att ctg cta ttt gag gct cag cac agc cag	1458
Val Leu Val Val Leu Gly Ile Leu Leu Phe Glu Ala Gln His Ser Gln	
445 450 455	
aga agc cta caa gat gca gcc ggg agg tga acagcagaga ggacaatgca	1508
Arg Ser Leu Gln Asp Ala Ala Gly Arg	
460 465	
tacttcagcg tgggtggagcc tcagggacag atctgatgat cccaggaggc tctggaggac	1568

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aatctaggac ctacattatc tggactgtat gctgggtcatt tctagagaca gcaatcaata 1628
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 tttttgtc 1696

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 <211> 466
 <212> PRT
 <213> Homo sapiens

<400> 31

Met Thr Pro Ile Leu Thr Val Leu Ile Cys Leu Gly Leu Ser Leu Gly
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Pro Arg Thr His Val Gln Ala Gly His Leu Pro Lys Pro Thr Leu Trp
 20 25 30

Ala Glu Pro Gly Ser Val Ile Ile Gln Gly Ser Pro Val Thr Leu Arg
 35 40 45

Cys Gln Gly Ser Leu Gln Ala Glu Glu Tyr His Leu Tyr Arg Glu Asn
 50 55 60

Lys Ser Ala Ser Trp Val Arg Arg Ile Gln Glu Pro Gly Lys Asn Gly
 65 70 75 80

Gln Phe Pro Ile Pro Ser Ile Thr Trp Glu His Ala Gly Arg Tyr His
 85 90 95

Cys Gln Tyr Tyr Ser His Asn His Ser Ser Glu Tyr Ser Asp Pro Leu
 100 105 110

Glu Leu Val Val Thr Gly Ala Tyr Ser Lys Pro Thr Leu Ser Ala Leu
 115 120 125

Pro Ser Pro Val Val Thr Leu Gly Gly Asn Val Thr Leu Gln Cys Val
 130 135 140

Ser Gln Val Ala Phe Asp Gly Phe Ile Leu Cys Lys Glu Gly Glu Asp
 145 150 155 160

Glu His Pro Gln Arg Leu Asn Ser His Ser His Ala Arg Gly Trp Ser
 165 170 175

Trp Ala Ile Phe Ser Val Gly Pro Val Ser Pro Ser Arg Arg Trp Ser
 180 185 190

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Tyr Arg Cys Tyr Ala Tyr Asp Ser Asn Ser Pro Tyr Val Trp Ser Leu
 195 200 205

Pro Ser Asp Leu Leu Glu Leu Leu Val Pro Gly Val Ser Lys Lys Pro
 210 215 220

Ser Leu Ser Val Gln Pro Gly Pro Met Val Ala Pro Gly Glu Ser Leu
 225 230 235 240

Thr Leu Gln Cys Val Ser Asp Val Gly Tyr Asp Arg Phe Val Leu Tyr
 245 250 255

Lys Glu Gly Glu Arg Asp Phe Leu Gln Arg Pro Gly Trp Gln Pro Gln
 260 265 270

Ala Gly Leu Ser Gln Ala Asn Phe Thr Leu Gly Pro Val Ser Pro Ser
 275 280 285

His Gly Gly Gln Tyr Arg Cys Tyr Ser Ala His Asn Leu Ser Ser Glu
 290 295 300

Trp Ser Ala Pro Ser Asp Pro Leu Asp Ile Leu Ile Thr Gly Gln Phe
 305 310 315 320

Tyr Asp Arg Pro Ser Leu Ser Val Gln Pro Val Pro Thr Val Ala Pro
 325 330 335

Gly Lys Asn Val Thr Leu Leu Cys Gln Ser Arg Gly Gln Phe His Thr
 340 345 350

Phe Leu Leu Thr Lys Glu Gly Ala Gly His Pro Pro Leu His Leu Arg
 355 360 365

Ser Glu His Gln Ala Gln Gln Asn Gln Ala Glu Phe Arg Met Gly Pro
 370 375 380

Val Thr Ser Ala His Val Gly Thr Tyr Arg Cys Tyr Ser Ser Leu Ser
 385 390 395 400

Ser Asn Pro Tyr Leu Leu Ser Leu Pro Ser Asp Pro Leu Glu Leu Val
 405 410 415

Val Ser Ala Ser Leu Gly Gln His Pro Gln Asp Tyr Thr Val Glu Asn
 420 425 430

Leu Ile Arg Met Gly Val Ala Gly Leu Val Leu Val Val Leu Gly Ile

•

435 440 445

Leu Leu Phe Glu Ala Gln His Ser Gln Arg Ser Leu Gln Asp Ala Ala
450 455 460

Gly Arg
465